



STIC Search Report

Biotech-Chem Library

Rapm Rapm

STIC Database Tracking Number: 110859

TO: Georgia L Helmer
Location: CM1/9B12/9D14
Art Unit: 1638
Tuesday, December 23, 2003

Case Serial Number: 09/289346

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Helmer,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

An pending
files
Removed
Dec 23, 2003

10 - OK
2 tie
3
4
5
6

7
8
9
-

Hart, Edward

110859

From: STIC-Biotech/ChemLib
Sent: Tuesday, December 23, 2003 8:47 AM
To: Hart, Edward
Subject: FW: Rush seq search--US09/289,346

-----Original Message-----

From: Chan, Christina
Sent: Tuesday, December 23, 2003 7:59 AM
To: Helmer, Georgia; STIC-Biotech/ChemLib
Subject: RE: Rush seq search--US09/289,346

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Helmer, Georgia
Sent: Monday, December 22, 2003 3:16 PM
To: Chan, Christina
Subject: Rush seq search--US09/289,346

Could you please do a sequence search of SEQ ID Nos 2-10 of case US 09/289,346.

Thanks in advance!

Georgia Helmer PhD
Patent Examiner - art unit 1638
(703) 308-7023
CM1 - 9D14
mailbox 9312

After 6 January 2004,
Phone (571) 272-0796
Office: Remson 2C15

12/23/03
ABSSP
9-AA



STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art found, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not** found:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds
(without alignments)
340.128 Million cell updates/sec

Title: US-09-289-346B-10
Perfect score: 364
Sequence: 1)TLVWGFQVDRSARGCQT.....FQFHLNLSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	364	100.0	70	21	AA198686
2	349	95.9	70	21	AA198677
3	349	95.9	356	21	AA198687
4	341	93.7	70	21	AA198685
5	338	92.9	70	21	AA198688
6	337	92.6	70	21	AA198692
7	335	92.0	70	21	AA198684
8	335	92.0	70	21	AA198690
9	334	91.8	70	21	AA198678

10	333	91.5	70	21	AA198689
11	331	90.9	70	21	AA198680
12	331	90.9	70	21	AA198691
13	328	90.1	70	21	AA198681
14	327	89.8	70	21	AA198683
15	325	89.3	70	21	AA198682
16	317	87.1	70	21	AA198679
17	223	61.3	353	18	AAW34338
18	223	61.3	353	18	AAW34332
19	223	61.3	353	18	AAW34333
20	223	61.3	353	18	AAW34334
21	223	61.3	353	18	AAW34335
22	221	60.7	353	8	AAF70407
23	221	60.7	359	17	AAW34326
24	221	60.7	359	17	AAW34327
25	221	60.7	359	17	AAW34328
26	221	60.7	361	18	AAW34329
27	221	60.7	361	18	AAW34330
28	221	60.7	361	18	AAW34331
29	221	60.7	361	18	AAW34332
30	212.5	58.4	361	8	AAF70562
31	208.5	57.3	50	23	AAO22043
32	207	56.9	362	19	AAW56495
33	206	56.6	357	18	AAW34329
34	206	56.6	357	18	AAW34330
35	206	56.6	357	18	AAW34331
36	198	54.4	357	18	AAW34337
37	95	26.1	142	24	ABP58120
38	68	18.7	857	23	ABP62804
39	65.5	18.0	945	22	ABW65231
40	65	17.9	292	21	AAV92317
41	65	17.9	335	21	AAV92318
42	64.5	17.7	665	22	ABW70991
43	64	17.6	712	23	AAU82975
44	64	17.6	722	23	ABP73316
45	63.5	17.4	163	21	AAW60400

ALIGNMENTS

RESULT 1

AA198686

ID AA198686 standard; peptide; 70 AA.

AC AA198686;

XX 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX Genminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

XX Tomato golden mosaic virus.

XX Key Location/Qualifiers

XX Misc-difference 24 /note= "wild type residue replaced with Leu"

XX Misc-difference 25 /note= "wild type residue replaced with Leu"

XX Misc-difference 26 /note= "wild type residue replaced with Leu"

XX WO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX PI WPI; 2000-618851/59.
 XX DR Transgenic plants with increased resistance to geminivirus infection
 XX PT comprise a nucleic acid construct containing a nucleic acid sequence
 XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX PT -
 XX PS Claim 53; Page 46; 73pp; English.
 XX CC The present sequence represents a mutant peptide, derived from a
 XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 XX CC protein are used to produce transgenic plants. The mutation in AL1 is
 XX CC present in a ribosome binding region, and expression of mutant AL1
 XX CC protein imparts increased resistance to geminivirus infection in the
 XX CC plant. Mutant AL1 proteins are useful for producing plants having
 XX CC increased resistance or reduced sensitivity to a geminivirus such as
 XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 XX CC virus, cotton leaf curl virus or beet curly top virus.
 XX SQ Sequence 70 AA;
 Query Match 100.0%; Score 364; DB 21; Length 70;
 Best Local Similarity 100.0%; Pred. No. 1.6e-38;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
 Db 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 Db 61 DRIFDKTPEP 70
 RESULT 2
 AAB18677
 ID AAB18677 standard; peptide; 70 AA.
 XX AC AAB18677;
 XX DT 22-JAN-2001 (first entry)
 XX DE Peptide fragment from Rep protein of TGMV (amino acids 110-179).
 XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 XX KW ribosome binding region; resistance; geminivirus infection.
 XX OS Tomato golden mosaic virus.
 XX PN WO200054573-A1.
 XX PD 21-SEP-2000.
 XX PF 15-MAR-2000; 2000WO-US06759.
 XX PR 18-MAR-1999; 99US-0125004.
 XX PR 09-APR-1999; 99US-0289346.
 XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX DR WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection
 XX PT comprise a nucleic acid construct containing a nucleic acid sequence
 XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX PT -
 XX PS Disclosure; Page 18; 73pp; English.
 XX CC The present sequence is derived from a geminivirus replication (Rep)
 XX CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
 XX CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
 XX CC with other viral and host proteins. Mutants of the AL1 protein are used
 XX CC to produce transgenic plants. The mutation in AL1 is present in a
 XX CC ribosome binding region, and expression of mutant AL1 protein imparts
 XX CC increased resistance to geminivirus infection in the plant. Mutant AL1
 XX CC proteins are useful for producing plants having increased resistance or
 XX CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
 XX CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 XX CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
 XX CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
 XX CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 XX CC beet curly top virus.
 XX SQ Sequence 70 AA;
 Query Match 95.9%; Score 349; DB 21; Length 70;
 Best Local Similarity 95.7%; Pred. No. 1.3e-36;
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
 Db 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 Db 61 DRIFDKTPEP 70
 RESULT 3
 AAB18687
 ID AAB18687 standard; peptide; 356 AA.
 XX AC AAB18687;
 XX DT 22-JAN-2001 (first entry)
 XX DE Amino acid sequence of a geminivirus replication protein of TGMV.
 XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 XX KW ribosome binding region; resistance; geminivirus infection.
 XX OS Tomato golden mosaic virus.
 XX PH Key Location/Qualifiers
 XX FT Misc-difference 354
 XX FT /note= "unspecified amino acid"
 XX PN WO200054573-A1.
 XX PD 21-SEP-2000.
 XX PF 15-MAR-2000; 2000WO-US06759.
 XX PR 18-MAR-1999; 99US-0125004.
 XX PR 09-APR-1999; 99US-0289346.
 XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX DR WPI; 2000-618851/59.
 XX PT Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
PS Disclosure; Page 47-48; 73pp; English.
XX
CC The present sequence represents a geminivirus replication (Rep)
CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
CC catalyses cleavage and ligation of single-stranded DNA, and interacts
CC with other viral and host proteins. Mutants of the AL1 protein are used
CC to produce transgenic plants. The mutation in AL1 is present in a
CC ribosome binding region, and expression of mutant AL1 protein imparts
CC increased resistance to geminivirus infection in the plant. Mutant AL1
CC proteins are useful for producing plants having increased resistance or
CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
XX beet curly top virus.
XX
SQ Sequence 356 AA;
Query Match 95.9%; Score 349; DB 21; Length 356;
Best Local Similarity 95.7%; Pred. No. 1e-35; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGFEVDGRSARGCGQTSNDLLLEALNASSKEEALQIIRKIPKYLFPQHNLNSNL 60
DB 110 TLVWGFEVDGRSARGCGQTSNDAAEALNASSKEEALQIIRKIPKYLFPQHNLNSNL 169
QY 61 DRIFDKTPEP 70
DB 170 DRIFDKTPEP 179
RESULT 4
AAB18685
ID AAB18685 standard; peptide; 70 AA.
AC AAB18685;
XX
XX 22-JAN-2001 (first entry)
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
OS Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 10 /note= "wild type residue replaced with Ala"
FT Misc-difference 19 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX
XX (UYN-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
PS Claim 53; Page 46; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX
SQ Sequence 70 AA;
Query Match 93.7%; Score 341; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 1.3e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TLVWGFEVDGRSARGCGQTSNDLLLEALNASSKEEALQIIRKIPKYLFPQHNLNSNL 60
DB 1 TLVWGFEVDGRSARGCGQTSNDAAEALNASSKEEALQIIRKIPKYLFPQHNLNSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 5
AAB18688
ID AAB18688 standard; peptide; 70 AA.
XX
AC AAB18688;
XX
XX 22-JAN-2001 (first entry)
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
OS Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 19 /note= "wild type residue replaced with Ala"
FT Misc-difference 20 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX
XX (UYN-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection

XX
XX

DR WPI: 2000-619851/59.

XX Transgenic plants with increased resistance to geminivirus infection

XX comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant Al1 protein with a mutation in the Rb binding region

XX

XX Disclosure: Page 49; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a

CC geminivirus replication (Rep) protein, also known as Al1. Al1 binds

CC double-stranded DNA, catalyses cleavage and ligation of single-stranded

CC DNA, and interacts with other viral and host proteins. Mutants of the

CC protein are used to produce transgenic plants. The mutation in Al1 is

CC present in a ribosome binding region, and expression of mutant Al1

CC protein imparts increased resistance to geminivirus infection in the

CC plant. Mutant Al1 proteins are useful for producing plants having

CC increased resistance or reduced sensitivity to a geminivirus such as

CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf

CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian

CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper

CC virus, cotton leaf curl virus or beet curly top virus.

XX

XX Sequence 70 AA:

SO

	Sequence	70 Aa,
	Query Match	92.0%; Score 335; DB 21; Length 70;
	Best Local Similarity	92.9%; Pred. No. 7.8e-35;
	Matches	65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY	1 TLVWGFSQVDGRSARGGCQTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLNSL	60
Dd	1 TLVWGFQVDGRSARGGCQTSDNAAAAAASSKEEALQIIREKIPEKYLFOFHNLNSL	60
QY	61 DRIFOKTPEP	70
Dd	61 DRIFOKTPEP	70

RESULT 9	
AAB18678	
ID	AAB18678 standard; peptide; 70 AA.
XX	
AC	AAB18678;
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	Mutant peptide derived from amino acids 110-179 of Rep (Al1) protein.
XX	
KW	Geminivirus; replication protein; Rep protein; Al1; transgenic plant;
KW	ribosome binding region; resistance; geminivirus infection.
XX	
OS	Synthetic.
OS	Tomato golden mosaic virus.
XX	
Key	Location/Qualifiers
FT	Misc-difference 12
FT	/note= "wild type residue replaced with Ala"
FT	Misc-difference 13
FT	/note= "wild type residue replaced with Ala"
FT	Misc-difference 15
FT	/note= "wild type residue replaced with Ala"
XX	
WO	WO200054573-A1.
PN	
XX	
PD	21-SEP-2000.
XX	
PF	15-MAR-2000; 2000WO-US06759.
XX	
XX	18-MAR-1999; 99US-0125004.
PR	09-APR-1999; 99US-0289346.
XX	
XX	(UYNC-) UNIV NORTH CAROLINA STATE.)

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX XX WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX
 PS Claim 53; Page 42-43; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 91.8%; Score 334; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 1e-34;
 Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDCRSARGCCQTSNDLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
 Db 1 TLVWGFQVDCRSARGCCQTSNDLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 Db 61 DRIFDKTPEP 70
 RESULT 10
 AAB18689
 ID AAB18689 standard; peptide; 70 AA.
 AC AAB18689;
 XX 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 FH Misc-difference 22 /note= "wild type residue replaced with Ala"
 FT Misc-difference 23 /note= "wild type residue replaced with Ala"
 FT Misc-difference 23 /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 FN 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX

PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX
 DR WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX
 PS Disclosure; Page 48-49; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 91.5%; Score 333; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 1.4e-34;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDCRSARGCCQTSNDLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
 Db 1 TLVWGFQVDCRSARGCCQTSNDLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 Db 61 DRIFDKTPEP 70
 -RESULT 11
 AAB18680
 ID AAB18680 standard; peptide; 70 AA.
 AC AAB18680;
 XX 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 FH Misc-difference 42 /note= "wild type residue replaced with Ala"
 FT Misc-difference 43 /note= "wild type residue replaced with Ala"
 FT Misc-difference 44 /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 FN 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 XX


```

PR 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 52; Page 43-44; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 90.9%; Score 331; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 2.5e-34;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
Oy 1 TLVWGFQVDRSGRGCGCQTSNDLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60
Db 1 TLVWGFQVDRSGRGCGCQTSNDAAAEALNASSKEEALQIIRAAIPEKYLQFPHNLSNL 60
Oy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
XX
RESULT 12
AAB18691
ID AAB18691 standard; peptide; 70 AA.
XX
XX AAB18691;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 34 /note= "wild type residue replaced with Ala"
XX Misc-difference 35 /note= "wild type residue replaced with Ala"
XX Misc-difference 36 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Disclosure; Page 49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 90.9%; Score 331; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 2.5e-34;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
Oy 1 TLVWGFQVDRSGRGCGCQTSNDLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60
Db 1 TLVWGFQVDRSGRGCGCQTSNDAAAEALNASSKEEALQIIRAAIPEKYLQFPHNLSNL 60
Oy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
XX
RESULT 13
AAB18681
ID AAB18681 standard; peptide; 70 AA.
XX
XX AAB18681;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 47 /note= "wild type residue replaced with Ala"
XX Misc-difference 48 /note= "wild type residue replaced with Ala"
XX Misc-difference 49 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX

```

PN WO200054573-A1.
 XX 21-SEP-2000.
 PD 15-MAR-2000; 2000WO-US06759.
 PF 18-MAR-1999; 99US-0125004.
 PR 05-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX Claim 52; Page 44; 73pp; English.
 PS The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX SQ Sequence 70 AA;
 Query Match 30.1%; Score 328; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 6e-34;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDSRGSGCQTSNDLLLEALNASKEEALQIREKIPKYLPOFHNLSNL 60
 DB 1 TLVWGEFQVDSRGSGCQTSNDAAAEALNASKEEALQIREKIPAAALPOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 14
 AAB18683
 ID AAB18683 standard; peptide; 70 AA.
 AC AAB18683;
 XX 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 PH Misc-difference 59
 FT /note= "wild type residue replaced with Ala"
 FT Misc-difference 61
 FT /note= "wild type residue replaced with Ala"

FT Misc-difference 62
 FT /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 XX 21-SEP-2000.
 PD 15-MAR-2000; 2000WO-US06759.
 PF 18-MAR-1999; 99US-0125004.
 PR 05-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX Claim 53; Page 45; 73pp; English.
 PS The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX SQ Sequence 70 AA;
 Query Match 89.8%; Score 327; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 8.1e-34;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDSRGSGCQTSNDLLLEALNASKEEALQIREKIPKYLPOFHNLSNL 60
 DB 1 TLVWGEFQVDSRGSGCQTSNDAAAEALNASKEEALQIREKIPKYLPOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 AAFDKTPEP 70
 RESULT 15
 AAB18682
 ID AAB18682 standard; peptide; 70 AA.
 XX AAB18682;
 XX 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 PH Misc-difference 52

FT /note= "wild type residue replaced with Ala"
 FT Misc-difference 54
 FT /note= "wild type residue replaced with Ala"
 FT Misc-difference 55
 FT /note= "wild type residue replaced with Ala"

XX
 PN WO200054573-Al.

XX
 PD 21-SEP-2000.

XX
 PF 15-MAR-2000; 2000WO-US06759.

XX
 PR 18-MAR-1999; 99US-0125004.

XX
 PR 09-APR-1999; 99US-0289346.

XX
 PA (UYN-) UNIV NORTH CAROLINA STATE.

XX
 PI Hanley-Bowdoin L, Orozco BM, Kong L;

XX
 DR WPI; 2000-618851/59.

XX
 PS Transgenic plants with increased resistance to geminivirus infection
 CC comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant ALI protein with a mutation in the Rb binding region
 PT
 PT

XX
 Claim 53; Page 44-45; 73pp; English.

XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.

XX
 SQ Sequence 70 AA;

Query Match 89.3%; Score 325; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred No. 1.4e-33;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGQTSNDLLLEALNASSKEEALQIIREKIPEKYLQFHLNLSNL 60

Db 1 TLVWGEFQVDRSARGGQTSNDLLLEALNASSKEEALQIIREKIPEKYLQFHLNLSNL 60

QY 61 DRIFDKTREP 70

Db 61 DRIFDKTREP 70

Search completed: December 23, 2003, 08:56:32
 Job time : 33.6667 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
1	223	61.3	353	3	US-08-838-151A-44	Sequence 44, Appl	
2	223	61.3	353	3	US-08-838-151A-46	Sequence 46, Appl	
3	223	61.3	353	3	US-08-838-151A-43	Sequence 49, Appl	
4	223	61.3	353	3	US-08-838-151A-52	Sequence 55, Appl	
5	223	61.3	353	3	US-08-838-151A-55	Sequence 2, Appl	
6	221	60.7	359	3	US-08-809-103B-2	Sequence 4, Appl	
7	221	60.7	359	3	US-08-809-103B-4	Sequence 6, Appl	
8	221	60.7	359	3	US-08-809-103B-6	Sequence 8, Appl	
9	221	60.7	359	3	US-08-809-103B-8	Sequence 2, Appl	
10	221	60.7	361	3	US-08-838-151A-2	Sequence 4, Appl	
11	221	60.7	361	3	US-08-838-151A-4	Sequence 6, Appl	
12	221	60.7	361	3	US-08-838-151A-6	Sequence 8, Appl	
13	221	60.7	361	3	US-08-838-151A-8	Sequence 24, Appl	
14	206	56.6	357	3	US-08-838-151A-24	Sequence 27, Appl	
15	206	56.6	357	3	US-08-838-151A-27	Sequence 30, Appl	
16	206	56.6	357	3	US-08-838-151A-30	Sequence 3, Appl	
17	198	54.4	357	3	US-08-838-151A-20	Sequence 6, Appl	
18	65	17.9	293	4	US-09-414-276-3	Sequence 3, Appl	
19	65	17.9	335	4	US-09-414-276-6	Sequence 6, Appl	
20	62.5	17.2	244	4	US-09-328-352-4541	Sequence 4541, Appl	
21	62	17.0	166	4	US-09-134-001C-3657	Sequence 3657, Appl	
22	61	16.8	602	2	US-08-419-652-6	Sequence 6, Appl	
23	61	16.8	771	1	US-07-923-976-6	Sequence 6, Appl	
24	61	16.8	783	6	5422248-2	Patent No. 5422248	
25	61	16.8	836	1	US-07-923-976-4	Sequence 4, Appl	
26	61	16.8	831	3	US-07-923-976-8	Sequence 8, Appl	
27	60.5	16.6	131	3	US-08-838-151A-14	Sequence 14, Appl	

Db 110 TIWGFQVQDGRSARGGQSSANDSYAKALNADSISSALTILKEQPKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70
:|||||

Db 170 ERIFVKVPEP 179

RESULT 2
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; TITLE OF INVENTION: Genes
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5400
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-46

Query Match 61.3%; Score 223; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 2.5e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGFQVQDGRSARGGQSSANDSYAKALNADSISSALTILKEQPKDYVLQHHNIRSNL 60
:|||||

Db 110 TIWGFQVQDGRSARGGQSSANDSYAKALNADSISSALTILKEQPKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70
:|||||

Db 170 ERIFVKVPEP 179

RESULT 3
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul

; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5400
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-49

Query Match 61.3%; Score 223; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 2.5e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGFQVQDGRSARGGQSSANDSYAKALNADSISSALTILKEQPKDYVLQHHNIRSNL 60
:|||||

Db 110 TIWGFQVQDGRSARGGQSSANDSYAKALNADSISSALTILKEQPKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70
:|||||

Db 170 ERIFVKVPEP 179

RESULT 4
US-08-838-151A-52
; Sequence 52, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-52

Query Match 61.3%; Score 223; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 2.5e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLQFPHNLNSL 60
Db 110 TIWGFQVDGRSARGGCGQSANDSYAKALNADSIESTILKEQPKDYVLQHNRNSL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 5
US-08-838-151A-55
; Sequence 55, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; APPLICATION NUMBER: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: protein
; US-08-838-151A-55

Query Match 61.3%; Score 223; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 2.5e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLQFPHNLNSL 60
Db 110 TIWGFQVDGRSARGGCGQSANDSYAKALNADSIESTILKEQPKDYVLQHNRNSL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 6
US-08-809-103B-2
; Sequence 2, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELE: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-2

Query Match 60.7%; Score 221; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 4.8e-21;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGFQVDGRSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLQFPHNLNSL 61
Db 111 LEWGTFOIDGRSARGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170

QY 62 RIFDKTPEP 70
Db 171 ERIFVKVPEP 179
```

Tue Dec 23 09:55:20 2003

us-09-289-346b-10.ra1

Db 171 KVFQVPPAP 179

RESULT 7

US-08-809-103B-4
; Sequence 4, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-4

Query Match 50.7%; Score 221; DB 3; Length 359;

Best Local Similarity 56.5%; Pred. No. 4.8e-21;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGEFQVDRSARGGCGTNDLLEALNASSKEEALQIIREKIPEKYLFPQHNLNSLD 61
Db 111 LEWGTFTQIDGRSARGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170
Qy 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 8

US-08-809-103B-6
; Sequence 6, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-6

Query Match 60.7%; Score 221; DB 3; Length 359;

Best Local Similarity 56.5%; Pred. No. 4.8e-21;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGEFQVDRSARGGCGTNDLLEALNASSKEEALQIIREKIPEKYLFPQHNLNSLD 61
Db 111 LEWGTFTQIDGRSARGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170
Qy 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 9

US-08-809-103B-8
; Sequence 8, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:

; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B

FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-8
Query Match 60.7%; Score 221; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 4.8e-21;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
QY 2 LVWGFQVDGRSARGGCGTSDNLLLEALNASSKEALQIREKIPEKYLQFPHNLSNL 61
Db 111 LEWGTQFQIDGRSARGGCGTANDAYAKAINAGSKQALDVKEIAPRDYVLHFNHNSNL 170
QY 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179
RESULT 10
US-08-838-151A-2
Sequence 2, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivrus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-2
Query Match 60.7%; Score 221; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 4.8e-21;
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;
QY 1 TLVWGFQVDGRSARGGCGTSDNLLLEALNASSKEALQIREKIPEKYLQFPHNLSNL 60
Db 110 TIWGFQIDGRSARGGCGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQHNIRSNL 169
QY 61 DRIEDKTPEP 70
Db 170 ERIFAKAPEP 179
RESULT 11
US-08-838-151A-4
Sequence 4, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivrus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-4
Query Match 60.7%; Score 221; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 4.8e-21;
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;
QY 1 TLVWGFQVDGRSARGGCGTSDNLLLEALNASSKEALQIREKIPEKYLQFPHNLSNL 60
Db 110 TIWGFQIDGRSARGGCGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQHNIRSNL 169


```
QY      61 DRIFDKTPEP 70
      :||| |
Db      170 ERIFAKAPEP 179

RESULT 12
US-08-838-151A-6
; Sequence 6, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; APPLICATION TYPE: protein
US-08-838-151A-6

Query Match      60.7%; Score 221; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 4.8e-21;
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY      1 TLVWGCFQVDRSGRGCGTSDNLLLEALNASKKEALQIREKIPEKYLFOFHNLSNL 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      110 TIWGDGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREEQKDFVLQNHIRSNL 169

QY      61 DRIFDKTPEP 70
      :||| |
Db      170 ERIFAKAPEP 179

RESULT 14
US-08-838-151A-24
; Sequence 24, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; APPLICATION TYPE: protein
US-08-838-151A-6

Query Match      60.7%; Score 221; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 4.8e-21;
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY      1 TLVWGCFQVDRSGRGCGTSDNLLLEALNASKKEALQIREKIPEKYLFOFHNLSNL 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      110 TIWGDGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREEQKDFVLQNHIRSNL 169

QY      61 DRIFDKTPEP 70
      :||| |
Db      170 ERIFAKAPEP 179

RESULT 13
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
```

```
/
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mueller, Lisa V
/ REGISTRATION NUMBER: 38,978
/ REFERENCE/DOCKET NUMBER: SVS3801P0260
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-616-5400
/ TELEFAX: 312-616-5460
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 357 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-838-151A-24

Query Match 56.6%; Score 206; DB 3; Length 357;
Best Local Similarity 63.9%; Pred. No. 4.6e-19;
Matches 39; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 4 WGEFQVDGSRARGGCGTNDLLLEALNASSKEEALQIIREKIPEKYLFOFHNLNSNLDRI 63
Db 111 FGVSDIGRSARGGQOSANDAYAEALNSGSKSEALNILEKAPKDYILOFHNLSSNLDRI 170
QY 64 F 64
Db 171 F 171

RESULT 15
US-08-838-151A-27
; Sequence 27, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-27
```

```
Query Match 56.6%; Score 206; DB 3; Length 357;
Best Local Similarity 63.9%; Pred. No. 4.6e-19;
Matches 39; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 4 WGEFQVDGSRARGGCGTNDLLLEALNASSKEEALQIIREKIPEKYLFOFHNLNSNLDRI 63
Db 111 FGVSDIGRSARGGQOSANDAYAEALNSGSKSEALNILEKAPKDYILOFHNLSSNLDRI 170
QY 64 F 64
Db 171 F 171

Search completed: December 23, 2003, 08:59:36
Job time : 12.6667 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds
(without alignments)
172.015 Million cell updates/sec

Title: US-09-289-346B-10

Perfect score: 364

Sequence: 1 TLVWGEFQVDSRGSGCQT.....FQFHNLSNLDRIKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/FCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	364	100.0	70	10	US-09-289-346A-10
2	349	95.9	70	10	US-09-289-346A-1
3	349	95.9	356	10	US-09-289-346A-11
4	341	93.7	70	10	US-09-289-346A-9
5	338	92.9	70	10	US-09-289-346A-12
6	337	92.6	70	10	US-09-289-346A-16
7	335	92.0	70	10	US-09-289-346A-8
8	335	92.0	70	10	US-09-289-346A-14
9	334	91.8	70	10	US-09-289-346A-2
10	333	91.5	70	10	US-09-289-346A-13
11	331	90.9	70	10	US-09-289-346A-4
12	331	90.9	70	10	US-09-289-346A-15
13	328	90.1	70	10	US-09-289-346A-5
14	327	89.8	70	10	US-09-289-346A-7
15	325	89.3	70	10	US-09-289-346A-6

16	317	87.1	70	10	US-09-289-346A-3	Sequence 3, Appli
17	65	17.9	293	15	US-10-151-336-3	Sequence 3, Appli
18	65	17.9	335	15	US-10-151-336-6	Sequence 6, Appli
19	65	17.9	886	15	US-10-156-761-9112	Sequence 9112, Ap
20	64	17.6	712	11	US-09-893-519A-35	Sequence 35, Appl
21	64	17.6	722	12	US-10-032-585-7153	Sequence 7153, Ap
22	63	17.3	343	9	US-09-815-242-10474	Sequence 10474, A
23	62	17.0	21	10	US-09-984-056-17	Sequence 17, Appl
24	62	17.0	21	10	US-09-984-057-17	Sequence 17, Appl
25	62	17.0	21	12	US-10-105-232-17	Sequence 17, Appl
26	62	17.0	21	12	US-10-189-437-17	Sequence 17, Appl
27	62	17.0	272	9	US-09-804-969-19	Sequence 19, Appl
28	62	17.0	340	10	US-09-835-936A-19	Sequence 19, Appl
29	62	17.0	340	12	US-10-094-749-2976	Sequence 2976, Ap
30	62	17.0	567	10	US-09-835-936A-8	Sequence 8, Appli
31	62	17.0	759	15	US-10-258-860-6	Sequence 6, Appli
32	62	17.0	762	9	US-09-804-969-15	Sequence 15, Appl
33	62	17.0	762	10	US-09-908-664-2	Sequence 2, Appli
34	62	17.0	762	15	US-10-258-860-2	Sequence 4, Appli
35	62	17.0	785	15	US-10-258-860-4	Sequence 27, Appl
36	61.5	16.9	1279	12	US-09-882-227-388	Sequence 388, App
37	61	16.8	603	12	US-10-071-962-27	Sequence 27, Appli
38	61	16.8	836	11	US-09-972-708-9	Sequence 369, App
39	60.5	16.6	447	9	US-09-989-723-369	Sequence 369, App
40	60.5	16.6	447	9	US-09-989-723-369	Sequence 369, App
41	60.5	16.6	447	9	US-09-989-723-369	Sequence 369, App
42	60.5	16.6	447	9	US-09-989-723-369	Sequence 369, App
43	60.5	16.6	447	10	US-09-989-731-369	Sequence 369, App
44	60.5	16.6	447	10	US-09-989-732-369	Sequence 369, App
45	60.5	16.6	447	10	US-09-991-073-369	Sequence 369, App

ALIGNMENTS

RESULT 1

US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; CURRENT APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LIL136).
US-09-289-346A-10

Query Match	100.0%;	Score 364;	DB 10;	Length 70;
Best Local Similarity	100.0%;	Pred. No. 4.4e-39;		
Matches	70;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
Oy	1	TLVWGEFQVDSRGSGCQTSNLLLEALNASSKEALQIRKIKPKYLFQFHNLSNL	60	
Db	1	TLVWGEFQVDSRGSGCQTSNLLLEALNASSKEALQIRKIKPKYLFQFHNLSNL	60	
Oy	61	DRIFDKTPPEP	70	

Best Local Similarity 92.9%; Pred. No. 9.4e-36;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
DB 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 6
US-09-289-346A-16
; Sequence 16, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-16

Query Match 92.6%; Score 337; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.3e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
DB 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 7
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of

OTHER INFORMATION: TMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->A118).
US-09-289-346A-8

Query Match 92.0%; Score 335; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.3e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
DB 1 TLVWGEAAVDGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 8
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match 92.0%; Score 335; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.3e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
DB 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 9
US-09-289-346A-2
; Sequence 2, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT

```

; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
US-09-289-346A-2

Query Match          91.8%; Score 334; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 3.1e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGCQTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60
Db 1 TLVWGEFQVDRSARGGCQTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-13

Query Match          91.5%; Score 333; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 4.1e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGCQTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60
Db 1 TLVWGEFQVDRSARGGCQTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18

```

```

; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (42)..(44)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAA154).
US-09-289-346A-4

Query Match          90.9%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 7.4e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGCQTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60
Db 1 TLVWGEFQVDRSARGGCQTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match          90.9%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 7.4e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGCQTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60
Db 1 TLVWGEFQVDRSARGGCQTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS

```

```
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (EKY159->AAAA159).
US-09-289-346A-5

Query Match          90.1%; Score 328; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.8e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCOTSDLLLEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
   |||||
Db 1 TLVWGEFQVDRSARGCGCOTSDAAAEALNASSKEEALQIIREKIPAAALQFPHNLNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 14
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDRI172->SALAA172).
US-09-289-346A-7

Query Match          89.8%; Score 327; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 2.4e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCOTSDLLLEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
   |||||
Db 1 TLVWGEFQVDRSARGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSAL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 AAIFDKTPEP 70
   |||||
```

```
RESULT 15
US-09-289-346A-6
; Sequence 6, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (52)..(55)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (QFHN165->AFAA165).
US-09-289-346A-6

Query Match          89.3%; Score 325; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 4.4e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCOTSDLLLEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
   |||||
Db 1 TLVWGEFQVDRSARGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

Search completed: December 23, 2003, 09:43:32
Job time : 77 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 seconds
(without alignments)
673.181 Million cell updates/sec

Title: US-09-289-346B-10
Perfect score: 364
Sequence: 1 TLVWGFQVDSRGSGCQR.....FQFHNLSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168692 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	349	95.9	352	1 QOCVLI	ALI protein - toma
2	249	68.4	361	1 QOCVPT	ALI protein - pota
3	242	66.5	358	2 S07594	hypothetical prote
4	235	64.6	362	1 JQ1887	ALI protein - toma
5	228	62.6	349	2 JQ2300	replicase - pepper
6	228	62.6	349	2 S31875	ALI protein - pepp
7	228	62.6	359	2 S39211	gene C1 protein -
8	221	60.7	359	2 S22593	hypothetical prote
9	220	60.4	355	1 QOCVW1	AVI protein - abut
10	218	59.9	351	2 JQ2327	ALI protein - indi
11	217	59.6	358	1 JQ1870	ALI protein - toma
12	217	59.6	385	2 S28360	ALI protein - beet
13	215	59.1	359	2 S39235	gene C1 protein -
14	208	57.1	360	2 S59885	replication-associ
15	206	56.6	357	1 QOCVC1	ALI protein - toma
16	138	37.9	131	2 S45059	AC1 protein (clone
17	125	34.3	347	1 QOCVS1	ALI protein - aqua
18	67	18.4	714	2 C95382	probable ferrichro
19	64	17.6	154	2 AD3475	protein-Npi-phosph
20	64	17.6	587	2 JQ1419	Fc gamma (IgG) rec
21	63.5	17.4	1229	2 T48959	kinesin-like prote
22	63	17.3	343	2 A98295	ribosomal RNA smal
23	63	17.3	343	2 C86136	probable enzyme yj
24	63	17.3	343	2 S56595	rRNA (guanine-N2-)
25	62	17.0	295	2 D42452	C1 protein - tobac
26	62	17.0	329	2 D85956	hypothetical prote
27	62	17.0	329	2 A91111	hypothetical prote
28	62	17.0	416	2 A82892	hypothetical prote
29	61.5	16.9	333	2 B42476	hypothetical prote

30 61.5 16.9 333 2 AC0766
31 61.5 16.9 481 2 A70091
32 61.5 16.9 1279 2 E64709
33 61 16.8 555 2 C45868
34 61 16.8 771 2 B38252
35 61 16.8 783 2 JH0329
36 61 16.8 863 2 C38252
37 60.5 16.6 447 2 T12544
38 60.5 16.6 1792 2 T13939
39 60 16.5 247 2 H86844
40 60 16.5 470 2 T46814
41 60 16.5 470 2 B95419
42 60 16.5 799 2 T48889
43 60 16.5 1117 2 T14891
44 60 16.5 1265 2 T02131
45 59.5 16.3 79 1 A58656

probable glycosylt
probable phosphoe
type IIS restricti
glycerol-3-phospha
granulocyte colony
granulocyte colony
granulocyte colony
hypothetical prote
myosin V - fruit f
glutamine ABC tran
gamma-aminobutyrat
diaminobutyrate-py
serine/threonine p
telomerase (EC 2.7
hypothetical prote
adipokinetic hormo

ALIGNMENTS

RESULT 1

QOCVLI
ALI protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994
C:Accession: A04170
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
C:Residues: 1-352 <HAM>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 95.9%; Score 349; DB 1; Length 352;
Best Local Similarity 95.7%; Pred. No. 1.7e-31;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TLVWGFQVDSRGSGCQTSNDLLLEALNASKKEALQIIREKIPEKYLFOFHNLSNL 60
Db 111 TLVWGFQVDSRGSGCQTSNDAAEALNASKKEALQIIREKIPEKYLFOFHNLSNL 170
Qy 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180

RESULT 2

QOCVPT
ALI protein - potato yellow mosaic virus (isolate Venezuela)
C:Species: potato yellow mosaic virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C:Accession: JU0364
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel
A:Reference number: JU0362; UID:91311403; PMID:1856690
A:Accession: JU0364
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-361 <COU>
A:Cross-references: GB:D00940; NID:G222458; PIDN:BAA00782.1; PID:G222459
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AL1 protein

A:Reference number: S39209

A:Accession: S39211

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-359 <NOR>

A:Cross-references: EMBL:Z25751; NID:q433655; PIDN:CAA81026.1; PID:q433658

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 62.6%; Score 228; DB 2; Length 359;

Best Local Similarity 59.4%; Pred. No. 6.9e-18; Indels 0; Gaps 0;

Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 2 LWGGEFQVDRSGRGCGTQTSNDLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNLD 61

DB 111 LEWTFQIDGSRGSGGQTANDAYAKAINAGSKSEALDVIKELAPRDYILHFHINSNLD 170

QY 62 RIFDKTPEP 70

DB 171 RVFQVPPAP 179

RESULT 8

S22593

Hypothetical protein C4 - tomato yellow leaf curl virus

C:Species: tomato yellow leaf curl virus

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999

C:Accession: S22593

R:Kheyr-Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.

Nucleic Acids Res. 19, 6763-6769, 1991

A:Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite

A:Reference number: S22588; MUID:92107660; PMID:1840676

A:Accession: S22593

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-359 <KHE>

A:Cross-references: EMBL:X61153; NID:G62211; PIDN:CAA43466.1; PID:G62217

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 60.7%; Score 221; DB 2; Length 359;

Best Local Similarity 56.5%; Pred. No. 4.2e-17; Indels 0; Gaps 0;

Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LWGGEFQVDRSGRGCGTQTSNDLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNLD 61

DB 111 LEWTFQIDGSRGSGGQTANDAYAKAINAGSKSQALDVIRELAPRDYILHFHINSNLD 170

QY 62 RIFDKTPEP 70

DB 171 RVFQVPPAP 179

RESULT 9

QOCVW1

AV1 protein - abutilon mosaic virus (isolate West India)

C:Species: abutilon mosaic virus

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Apr-1994

C:Accession: A36214

R:Frishmuth, T.; Zimmatt, G.; Jeske, H.

Virology 178, 461-468, 1990

A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as well

A:Reference number: A36214; MUID:91020984; PMID:2219703

A:Accession: A36214

A:Molecule type: DNA

A:Residues: 1-355 <PRI>

A:Cross-references: EMBL:X15993

C:Genetics:

C:Map position: segment A

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 60.4%; Score 220; DB 1; Length 355;

Best Local Similarity 58.6%; Pred. No. 5.4e-17; Indels 0; Gaps 0;

Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGTQTSNDLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNLD 60

DB 110 TAEWGEFQIDGSRGSGGQTANDSYAKALNAGDVQSALNILKEQPKDYVLQNHNRISNLD 169

QY 61 DRIFDKTPEP 70

DB 170 ERIFAKAPEP 179

RESULT 10

JQ2327

AL1 protein - Indian cassava mosaic virus

N:Alternate names: replication-associated protein

C:Species: Indian cassava mosaic virus

C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 20-Sep-1999

C:Accession: JQ2327; S35883

R:Hong, Y.G.; Robinson, D.J.; Harrison, B.D.

J. Gen. Virol. 74, 2437-2443, 1993

A:Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-tr

A:Reference number: JQ2326; MUID:94065670; PMID:8245859

A:Accession: JQ2327

A:Molecule type: DNA

A:Residues: 1-351 <HON>

A:Cross-references: EMBL:Z24758; NID:G395351; PIDN:CAA80891.1; PID:G584046

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.9%; Score 218; DB 2; Length 351;

Best Local Similarity 61.2%; Pred. No. 9e-17; Indels 0; Gaps 0;

Matches 41; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 4 WGEFQVDRSGRGCGTQTSNDLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNLDRI 63

DB 113 WGTFTQIDGSRGSGGQTANDAYAAALNSGSKILFELAPRDYILRFHHSNLDRI 172

QY 64 FDKTPEP 70

DB 173 FTXPPPP 179

RESULT 11

JQ1870

AL1 protein - tomato mottle virus (isolate Florida)

C:Species: tomato mottle virus

C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999

C:Accession: JQ1870

R:Abouzid, A.M.; Polston, J.E.; Hiebert, E.

J. Gen. Virol. 73, 3225-3229, 1992

A:Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated fr

A:Reference number: JQ1869; MUID:93107858; PMID:1469361

A:Accession: JQ1870

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-358 <ABO>

A:Cross-references: GB:114460

C:Genetics:

C:Map position: segment A

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.6%; Score 217; DB 1; Length 358;

Best Local Similarity 55.7%; Pred. No. 1.2e-16; Indels 0; Gaps 0;

Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGTQTSNDLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNLD 60

DB 107 TIWGEFQIDGSRGSGGQTANDSYAKALNAGSVQSALAVIREEQPKDYVLQNHNRISNLD 166

QY 61 DRIFDKTPEP 70

DB 167 ERIFAKAPEP 176

RESULT 12

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds
(without alignments)
569.747 Million cell updates/sec

Title: US-09-289-346B-10
Perfect score: 364
Sequence: 1 TLVWGEFQVDSARGGCQT.....QFHNLSNLDRIFDKTPPEP 70

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	349	95.9	352	1 VAL1_TGMV	P03567 tomato gold
2	249	68.4	361	1 VAL1_PYMV	P27258 potato yell
3	242	66.5	358	1 VAL1_CLV	P14982 cassava lat
4	242	66.5	358	1 VAL1_CLVN	P14972 cassava lat
5	235	64.6	362	1 VAL1_TYLCA	P36279 tomato yell
6	228	62.6	349	1 VAL1_PHVU	Q06923 pepper huas
7	228	62.6	359	1 VAL1_TYLCU	P38609 tomato yell
8	221	60.7	353	1 VAL1_BGMV	P05175 bean golden
9	221	60.7	359	1 VAL1_TYLCM	P27260 tomato yell
10	220	60.4	355	1 VAL1_ABMVM	P21947 abutilon mo
11	217	59.6	358	1 VAL1_BCTV	P14991 beet curly
12	217	59.6	361	1 VAL1_TMOV	Q06657 tomato mott
13	206	56.6	357	1 VAL1_TYLCV	P27259 tomato yell
14	125	34.3	347	1 VAL1_SLCV	P29048 squash leaf
15	63	17.3	342	1 RSMC_ECOLI	P39406 escherichia
16	62	17.0	150	1 DTD_STAEP	Q8CP01 staphylococ
17	62	17.0	295	1 VAL1_TYDVA	P1617 tobacco yell
18	62	17.0	387	1 YAPF_RHISN	P5615 rhizobium s
19	61	16.8	555	1 GLPD_EACSU	P18158 bacillus su
20	61	16.8	836	1 GCSR_HUMAN	Q99062 homo sapien
21	60.5	16.6	447	1 TBL2_HUMAN	Q9Y4P3 homo sapien
22	60	16.5	392	1 CL02_HUMAN	Q8NHQ8 homo sapien
23	60	16.5	470	1 RHA_RHIME	Q2Z3R2 r diaminobu
24	60	16.5	509	1 CA43_DROME	Q9VMS7 drosophila
25	60	16.5	799	1 AFSK_STRCO	P54741 streptomyc
26	60	16.5	807	1 AFSK_STRGR	P54742 streptomyc
27	60	16.5	1117	1 TERT_TETH	O77448 tetrahymena
28	59.5	16.3	79	1 AKHD_DROME	P17975 drosophila
29	58.5	16.1	323	1 VAL1_PASVK	Q00338 panicum str
30	58.5	16.1	397	1 METL_RAT	P13444 rattus norv
31	58.5	16.1	1610	1 CCAD_MESAU	Q99244 mesocricetu
32	58.5	16.1	2161	1 CCAD_HUMAN	Q01668 homo sapien
33	58.5	16.1	2203	1 CCAD_RAT	P27732 rattus norv

ALIGNMENTS

RESULT 1
ID VAL1_TGMV STANDARD; PRT; 352 AA.
AC P03567;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 25, Last annotation update)
DE All protein.
GN AC1.
OS Tomato golden mosaic virus (TGMV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
CX NCBI TaxID=10831;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;
RT "Complete nucleotide sequence of the infectious cloned DNA components
of tomato golden mosaic virus: potential coding regions and regulatory
sequences.";
RL EMBL J. 3:2197-2205 (1984).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
CC -----
EMBL: K02029; ; NOT_ANNOTATED_CDS.
PIR: A04170; Q0CVL1.
InterPro: IPR001191; Gemini_AL1.
Pfam: PF00799; Gemini_AL1; 1.
PRINTS: PR00227; GEMCOATALL.
ProDom: PD000736; Gemini_AL1; 1.
KW ATP-binding.
DR NP_BIND.
FT NP_BIND.
SQ SEQUENCE 352 AA; 40332 MW; C33C938E9644B4A4 CRC64;
Query Match 95.9%; Score 349; DB 1; Length 352;
Best Local Similarity 95.7%; Pred. No. 1.5e-31;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TLVWGEFQVDSARGGCQTSNDLLALNASSKEALQIIREKIPKYLQFHNLSNL 60
Db 111 TLVWGEFQVDSARGGCQTSNDAAALNASSKEALQIIREKIPKYLQFHNLSNL 170
Qy 61 DRIFDKTPPEP 70
Db 171 DRIFDKTPPEP 180
RESULT 2
ID VAL1_PYMV STANDARD; PRT; 361 AA.
AC P27258;

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE A1 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "the nucleotide sequence of the infectious cloned DNA components of
potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; D00940; BAA0782.1; -
DR PIR; J0364; QOCVPT.
DR InterPro; IPR001191; Gemini_A11.
DR Pfam; PF00799; Gemini_A11; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_A11; 1.
KW ATP-binding.
FT NP_BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 361 AA; 40950 MW; 5627A33BF1264383 CRC64;

Query Match 68.4%; Score 249; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 2.2e-20;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGQTNDLLLEALNASSKEALQIIREKIPKYLQFHNLSNL 60
DB 110 TIWGLFQIDGRSARGGCGQTNDAAALNSGTREAAWKIKELPKFLQFVHNLSNL 169
QY 61 DRIFDKTPE 69
DB 170 DRIFDKAPE 178

RESULT 3
VAL1 CLVK
ID VAL1 CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE A11 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC

CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_A11.
DR Pfam; PF00799; Gemini_A11; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_A11; 1.
KW ATP-binding.
FT NP_BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753EE92D69 CRC64;

Query Match 66.5%; Score 242; DB 1; Length 358;
Best Local Similarity 61.4%; Pred. No. 1.3e-19;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGQTNDLLLEALNASSKEALQIIREKIPKYLQFHNLSNL 60
DB 109 TIWGLFQIDGRSARGGCGQTNDAAALNSGTREAAWKIKELPKFLQFVHNLSNL 168
QY 61 DRIFDKTPE 70
DB 169 DRIFQEPAP 178

RESULT 4
VAL1 CLVN
ID VAL1 CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE A11 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
RL Nucleic Acids Res 18:197-198(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; X17095; CAA34953.1; -
DR PIR; S07594; S07594.
DR InterPro; IPR001191; Gemini_A11.
DR Pfam; PF00799; Gemini_A11; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_A11; 1.
KW ATP-binding.
FT NP_BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16BB0CB2D5E2C CRC64;

Query Match 66.5%; Score 242; DB 1; Length 358;
Best Local Similarity 61.4%; Pred. No. 1.3e-19;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGQTNDLLLEALNASSKEALQIIREKIPKYLQFHNLSNL 60
DB 109 TIWGLFQIDGRSARGGCGQTNDAAALNSGTREAAWKIKELPKFLQFVHNLSNL 168
QY 61 DRIFDKTPE 70
DB 169 DRIFQEPAP 178

```

RESULT 5
ID VAL1_TYLCU STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AL1 protein (C1 protein).
GN Cl..
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses: Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Rigden J.E., Krake L.R., Mullineaux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
geminivirus."
RL J. Gen. Virol. 74:147-151 (1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR PIR: JQ1887; JQ1887.
DR InterPro: IPR001191; Geminini_A11.
DR Pfam: PF00799; Geminini_A11; I.
DR PRINTS: PR00227; GEMCOATALL1.
DR ProDom: PD000736; Geminini_A11; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 64.6%; Score 235; DB 1; Length 362;
Best Local Similarity 54.1%; Pred. No. 8.1e-19;
Matches 46; Conservative 9; Mismatches 14; Indels 16; Gaps 1;

Qy 1 TLVGEFQVDRSGRGCGTSDLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
Db 110 TLEWGEFQIDGRSARGGQQSANDAYACALNTGSKSEALNVRLAPKDYVYLQFHNLSNL 169

Qy 61 DRI-----FDKTPPE 69
Db 170 DRIPTPELVVSPFLSSFDVRPE 194

RESULT 6
ID VAL1_PHVU STANDARD; PRT; 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN Al1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses: Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tirnado J.A., Herrera-Estrella L.,
RA Rivera-Sustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
comparison with bipartite geminiviruses."
RL J. Gen. Virol. 74:2225-2231 (1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z25751; CAA81026.1; --
CC PIR; S39211; S39211.
CC InterPro; IPR001191; Geminini_A11.
CC Pfam; PF00799; Geminini_A11; I.
CC PRINTS; PR00227; GEMCOATALL1.
CC ProDom; PD000736; Geminini_A11; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 349 AA; 41065 MW; 2D170A51EF80A3BC CRC64;

Query Match 62.6%; Score 228; DB 1; Length 359;
Best Local Similarity 59.4%; Pred. No. 4.8e-18;
Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LWVGEFQVDRSGRGCGTSDLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 61
Db 111 LEWGTFFQIDGRSARGGQQTANDAYAKAINAGSKSEALDVIKELAPRDYILHFHNLSNL 170

```

```

CC EMBL; X70418; CAA49856.1; --
CC PIR; JQ2300; JQ2300.
CC PIR; S31875; S31875.
CC InterPro; IPR001191; Geminini_A11.
CC Pfam; PF00799; Geminini_A11; I.
CC PRINTS; PR00227; GEMCOATALL1.
CC ProDom; PD000736; Geminini_A11; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 39722 MW; DSF4E76CD56370F4 CRC64;

Query Match 62.6%; Score 228; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 4.7e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDRSGRGCGTSDLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
Db 110 TVEWGEFQIDGRSARGGQQSANDTYAKALNSASAEALQIIRKQPQHFLOFHNIVSNA 169

Qy 61 DRIFDKTPPEP 70
Db 170 NRIFQTPPEP 179

RESULT 7
ID VAL1_TYLCU STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (C1 protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Norris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
RT from the west Mediterranean basin: the nucleotide sequence of an
RT infectious clone from Spain."
RL Arch. Virol. 135:165-170 (1994).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z25751; CAA81026.1; --
CC PIR; S39211; S39211.
CC InterPro; IPR001191; Geminini_A11.
CC Pfam; PF00799; Geminini_A11; I.
CC PRINTS; PR00227; GEMCOATALL1.
CC ProDom; PD000736; Geminini_A11; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3BC CRC64;

Query Match 62.6%; Score 228; DB 1; Length 359;
Best Local Similarity 59.4%; Pred. No. 4.8e-18;
Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LWVGEFQVDRSGRGCGTSDLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 61
Db 111 LEWGTFFQIDGRSARGGQQTANDAYAKAINAGSKSEALDVIKELAPRDYILHFHNLSNL 170

```

```

QY      62 RIFDKTPEP 70
DB      171 RVFQVPEP 179

RESULT 8
VAL1 BGWV
ID VAL1 BGWV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE AL1 protein (40.2 kDa protein).
GN AC1
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
  regulation in geminiviruses."
RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
CC -/- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X61153; CAA43466.1; -
CC PIR; S22593; S22593.
CC PDB; 1L2M; 18-SEP-02.
CC PDB; 1L5I; 18-SEP-02.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding; 3D-structure.
FT NP BIND 220 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 60.7%; Score 221; DB 1; Length 353;
Best Local Similarity 60.0%; Pred. No. 2.8e-17;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY      1 TLVWGQFQVDSRGSGCOTSNLLLEALNASSKEEALQIREKIPEKYLFOFHNLSNL 60
DB      110 TLVWGQFQVDSRGSGCOTSNLLLEALNASSKEEALQIREKIPEKYLFOFHNLSNL 169

QY      61 DRIEDKTPEP 70
DB      170 ERIFKVPPEP 179

RESULT 9
VAL1 TYLCM
ID VAL1 TYLCM STANDARD; PRT; 359 AA.
AC P27250;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92107660; PubMed=1840676;
RA Kheyx-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a
  whitefly-transmitted monopartite geminivirus."
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -/- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X61153; CAA43466.1; -
CC PIR; S22593; S22593.
CC PDB; 1L2M; 18-SEP-02.
CC PDB; 1L5I; 18-SEP-02.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding; 3D-structure.
FT NP BIND 220 229 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 40733 MW; 971B4A07C93EFA7 CRC64;

Query Match 60.7%; Score 221; DB 1; Length 359;
Best Local Similarity 56.5%; Pred. No. 2.9e-17;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY      2 LVWGQFQVDSRGSGCOTSNLLLEALNASSKEEALQIREKIPEKYLFOFHNLSNL 61
DB      111 LVWGQFQVDSRGSGCOTSNLLLEALNASSKEEALQIREKIPEKYLFOFHNLSNL 170

QY      62 RIFDKTPEP 70
DB      171 RVFQVPEP 179

RESULT 10
VAL1 ABMVV
ID VAL1 ABMVV STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimmatt G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
  as well as eukaryotic features."
RL Virology 178:461-468(1990).
CC -/- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X15983; -; NOT_ANNOTATED_CDS.
CC PIR; A36214; QOCVW1.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.

```



```

GN AL1.
OS Tomato mottle virus (isolate Florida) (TMoV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=36449;
NN
RN
RX SEQUENCE FROM N.A.
RE MEDLINE=93107850; PubMed=1469361;
RA Abouid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida.";
RL J. Gen. Virol. 73:3225-3229(1992).
CC
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L14460; AAC32414.1; -.
DR PIR; JQ1870; JQ1870.
DR InterPro; IPR001194; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOAT1.
DR PRODOM; PD000736; Gemini_AL1.1.
DR ATP-binding.
KW NP BIND 222 229 ATP (BY SIMILARITY).
FT SEQUENCE 361 AA; 40516 MW; 8138B65CEEAC6950 CRC64;
SQ
Query Match 59.6%; Score 217; DB 1; Length 361;
Best Local Similarity 55.7%; Pred. No. 8.2e-17;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDRSGCGCTSNLLLEALNASKKEALQIREKTPKYLQFQHNLSNL 60
Db 110 TLWGDQFDIGRSARGQQSQANDSYAKALNAGSVQSALAVLREQPKDFVLQNHNSNL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179
QY
Db
RESULT 13
VAL1_TYLCV
ID VAL1_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (Cl protein).
CL
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=10832;
RN [1]
RX SEQUENCE FROM N.A.
RE MEDLINE=92024070; PubMed=1926771;
RA Navot N., Fichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component.";
RL Virology 185:151-161(1991).
CC
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC

```



```

DR EMBL; X15856; CAA33688.1; -.
DR PIR; D40779; QOCVCI.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding. 219 226 ATP (POTENTIAL).
FT NP_BIND 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match 56.6%; Score 206; DB 1; Length 357;
Best Local Similarity 63.9%; Pred. No. 1.4e-15;
Matches 39; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 4 WGEFQVDSRGSGCQTNDLLLEALNASSKEEALQIIRKIPKYLQFPHNLSNLDRI 63
DB 111 FGVSQIDGSRGSGGQSQANDAYEALNGSKSEALNILKRAPIQYLFPHLSNLDRI 170

QY 64 F 64
DB 171 F 171

RESULT 14
VAL1_SLCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91082449; PubMed-1984668;
RA Lazarowitz S.G.; Lazdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic components of a bipartite squash leaf curl geminivirus with a broad host range phenotype."
RT Virology 180:58-69(1991).
RL [1]
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
DR EMBL; M38183; AAC32410.1; ALT_INIT.
DR PIR; C36785; QOCVSI.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding. 218 225 ATP (POTENTIAL).
FT NP_BIND 347 AA; 39110 MW; AFDABDE122110E CRC64;
SQ SEQUENCE 347 AA; 39110 MW; AFDABDE122110E CRC64;

Query Match 34.3%; Score 125; DB 1; Length 347;
Best Local Similarity 37.9%; Pred. No. 1.4e-06;
Matches 25; Conservative 15; Mismatches 22; Indels 4; Gaps 1;

QY 5 GEQFQVDSRGSGCQTNDLLLEALNASSKEEALQIIRKIPKYLQFPHNLSNLDRI 64
DB 116 GQYKVSQ----GSKSNKDDYTHNAVAGSAGEALDIKAGDKPTIVYVNHILANVERLF 171

QY 65 DKTPEP 70
DB 172 QKPEP 177

```

RESULT 15

```

RSMC_ECOLI STANDARD; PRT; 342 AA.
AC P39406;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosomal RNA small subunit methyltransferase C (EC 2.1.1.52) (rRNA (guanine-N(2)-methyltransferase) (16S rRNA m2G1207 methyltransferase)).
DE RSMC OR B4371.
GN Escherichia coli.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE-95334362; PubMed-7610040;
RA Burland V.D.; Plunkett G. III; Sofia H.J.; Daniels D.L.;
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes."
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [2]
RP SEQUENCE OF 1-19, AND CHARACTERIZATION.
RX MEDLINE-99091632; PubMed-9873033;
RA Tscherne J.S.; Nurse K.; Popienick P.; Ofengand J.;
RT "Purification, cloning, and characterization of the 16S RNA m2G1207 methyltransferase from Escherichia coli."
RL J. Biol. Chem. 274:924-929(1999).
CC -1- FUNCTION: SPECIFICALLY METHYLATES THE GUANOSINE IN POSITION 1207 OF 16S RNA IN THE 30S PARTICLE.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + rRNA = S-adenosyl-L-homocysteine + rRNA containing N(2)-methylguanine.
CC -1- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY. RSMC SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
DR EMBL; U14003; AAA97267.1; -.
DR EMBL; AE000507; AAC77324.1; -.
DR PIR; S56595; S56595.
DR EcoGene; EG12596; rsmc.
DR InterPro; IPR002296; N12N6_mtfase.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF05175; MTS_2.
DR PRINTS; PR00507; N12N6MTFRASE.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
KW rRNA processing; transferase; Methyltransferase; Magnesium; Complete proteome.
FT INIT_MET 0
SQ SEQUENCE 342 AA; 37493 MW; C7A318155700302D CRC64;

Query Match 17.3%; Score 63; DB 1; Length 342;
Best Local Similarity 31.1%; Pred. No. 11;
Matches 14; Conservative 7; Mismatches 16; Indels 8; Gaps 1;

QY 4 WGEFQVDSRGSGCQTNDLLLEALNASSKEEALQI 40
DB 158 WGEYSVDGLTVKTLPGVFSRDLGVDGSQLLLSTLTHTTKKVLDV 202

```

Tue Dec 23 09:55:21 2003

us-09-289-346b-10.rsp

Page 7

Search completed: December 23, 2003, 08:57:41
Job time : 6.77778 secs

[illegible]

DT	01-MAY-2000	(TrEMBLrel. 13, Created)
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)
DE	REP.	Replication associated protein (Fragment).
OS	Cowpea golden mosaic virus.	
OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.	
OX	NCBI_TaxID=69263;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CGMV-BR;	
RA	Faria J.C.;	
RT	"Partial nucleotide sequence of cowpea golden mosaic geminivirus from Brazil";	
RL	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL; AF188708; AAF06318.1; -	
DR	InterPro; IPR001191; Gemini_AL1.	
DR	Pfam; PF00799; Gemini_AL1; I.	
DR	PRINTS; PR00227; GEMCOATL1.	
DR	ProDom; PD000736; Gemini_AL1; 1.	
FT	NON TER 225	
SQ	SEQUENCE 225 AA; 25766 MW; 1089CB6BD8D15B5D CRC64;	
Query Match 76.8%; Score 279; DB 12; Length 225;		
Best Local Similarity 77.8%; Pred. No. 5.4e-24;		
Matches 52; Conservative 7; Mismatches 8; Indels 0; Gaps 0;		
QY	4	WGFEVQDGSRGARGCQTSDLLLEALNASSKEEALQIIREKIPKYLFQFHNLSNLDRI 63
Dd	113	WGHPQIDGRSARGSGQTINDAASEALNASSKEEAQIIKEKLPEKFLFYHNLSSNLDRI 172
QY	64	FDKTPEP 70
Dd	173	FKKPPEP 179
RESULT 8		
Q9ELT8 PRELIMINARY; PRT; 314 AA.		
ID	Q9ELT8	
AC	Q9ELT8;	
DT	01-MAR-2001	(TrEMBLrel. 16, Created)
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)
DE	REP.	Replication association protein.
OS	Ac1.	
OS	Sweet potato leaf curl virus.	
OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.	
OX	NCBI_TaxID=100755;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;	
RT	"Detection of a geminivirus infecting sweet potato in the United States.";	
RL	Plant Dis. 82:1253-1257(1998).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RA	Lotrakul P., Valverde R.A.;	
RL	Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL; AF288227; AAG01006.1; -	
DR	InterPro; IPR001191; Gemini_AL1.	
DR	Pfam; PF00799; Gemini_AL1; I.	
DR	PRINTS; PR00227; GEMCOATL1.	
DR	ProDom; PD000736; Gemini_AL1; 1.	
SQ	SEQUENCE 314 AA; 35153 MW; 686220613046943F CRC64;	
Query Match 76.1%; Score 277; DB 12; Length 314;		
Best Local Similarity 79.4%; Pred. No. 1.4e-23;		
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;		
QY	1	TLWGEFQVDGRGARGCQTSNDLLLEALNASSKEEALQIIREKIPKYLFQFHNLSNLI 60
Dd	110	TITWGEFQVDGRGARGQQQTANDAAAEALNASSKEAALQIIREKLPKYLFQFHNLSNI 169

```

QY      61 DRIFDKTP 68
Db      170 DRIFSPPP 177

RESULT 9
Q9Q555 PRELIMINARY; PRT; 364 AA.
AC Q9Q555;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RT virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0(1999).
DR EMBL; AF104036; A047173.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRODOM; PD000736; Geminini_AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 76.1%; Score 277; DB 12; Length 364;
Best Local Similarity 79.4%; Pred. No. 1.6e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY      1 TLVWGFEQVQDGRSARGGCGTQNDLLEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TITWGFQVQDGRSARGGCGTQNDLLEALNASSKEALQIIREKIPEKYLQFHNLSNL 169
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      61 DRIFDKTP 68
Db      170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA Roye M.E., McLaughlin W.A., Nakha N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed
RT species Sida spp, Macroptilium lathyroides, and Wissadula amplissima
RT from Jamaica.";
RL Plant Dis. 81:1251-1258(1997).
DR EMBL; U67926; AAB97865.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.

QY      1 TLVWGFEQVQDGRSARGGCGTQNDLLEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TITWGFQVQDGRSARGGCGTQNDLLEALNASSKEALQIIREKIPEKYLQFHNLSNL 169
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      61 DRIFDKTP 68
Db      170 DRIFSPPP 177

RESULT 11
Q8QPU4 PRELIMINARY; PRT; 235 AA.
AC Q8QPU4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RA Ribeiro S.G., Ambrozovicius L.P., de Avila A.C., Calegario R.F.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini P.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049208; AAL82833.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR PRODOM; PD000736; Geminini_AL1; 1.
DR NON TER 235 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BE0DDC810 CRC64;

Query Match 74.7%; Score 272; DB 12; Length 235;
Best Local Similarity 74.6%; Pred. No. 3.6e-23;
Matches 50; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY      4 WGEFQVQDGRSARGGCGTQNDLLEALNASSKEALQIIREKIPEKYLQFHNLSNL 63
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      113 WGIFQIDGRSARGGCGTQNDLLEALNASSKEALQIIREKIPEKYLQFHNLSNL 172
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      64 FDKTPEP 70
Db      173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

```


Search completed: December 23, 2003, 09:03:37
Job time : 25.3333 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds
(without alignments)
340.128 Million cell updates/sec

Title: US-09-289-346B-2

Perfect score: 162

Sequence: 1 TLVGFQVQDAAGGCGT.....FQFHNLSNLDRIEDKTPET 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB ID	Description
1	362	100.0	70 21 AAB18678	Mutant peptide der
2	349	96.4	70 21 AAB18677	Peptide fragment f
3	349	96.4	356 21 AAB18687	Amino acid sequenc
4	341	94.2	70 21 AAB18685	Mutant peptide der
5	338	93.4	70 21 AAB18688	Mutant peptide der
6	337	93.1	70 21 AAB18692	Mutant peptide der
7	335	92.5	70 21 AAB18684	Mutant peptide der
8	335	92.5	70 21 AAB18690	Mutant peptide der
9	334	92.3	70 21 AAB18686	Mutant peptide der

10	333	92.0	70 21 AAB18689	Mutant peptide der
11	331	91.4	70 21 AAB18680	Mutant peptide der
12	331	91.4	70 21 AAB18691	Mutant peptide der
13	328	90.6	70 21 AAB18681	Mutant peptide der
14	327	90.3	70 21 AAB18683	Mutant peptide der
15	325	89.8	70 21 AAB18682	Mutant peptide der
16	317	87.6	70 21 AAB18679	Mutant peptide der
17	233.5	61.7	50 23 AAO22043	Retinoblastoma-bin
18	215	59.4	353 18 AAW34338	Bean golden mosaic
19	215	59.4	353 18 AAW34332	Bean golden mosaic
20	215	59.4	353 18 AAW34333	Bean golden mosaic
21	215	59.4	353 18 AAW34334	Bean golden mosaic
22	215	59.4	353 18 AAW34335	Bean golden mosaic
23	215	59.4	359 17 AAR88870	Sardinian tomato Y
24	215	59.4	359 17 AAR88871	Sardinian tomato Y
25	215	59.4	359 17 AAR88872	Sardinian tomato Y
26	213	58.8	353 8 AAP70407	ORF 4 gene product
27	213	58.8	361 18 AAW34336	Tomato mottle viru
28	213	58.8	361 18 AAW34324	Tomato mottle viru
29	213	58.8	361 18 AAW34325	Tomato mottle viru
30	213	58.8	361 18 AAW34326	Tomato mottle viru
31	206.5	57.0	361 8 AAP70562	Product of ORF 4 f
32	201	55.5	362 19 AAW56495	Tobacco leaf curl
33	200	55.2	357 18 AAW34329	Tomato yellow leaf
34	200	55.2	357 18 AAW34330	Tomato yellow leaf
35	200	55.2	357 18 AAW34331	Tomato yellow leaf
36	192	53.0	357 18 AAW34337	Tomato yellow leaf
37	89	24.6	142 24 ABP58120	Tomato yellow leaf
38	81.5	22.5	945 22 ABB56231	Drosophila melanog
39	69.5	19.2	512 19 AAW68473	HIV-1 strain YBF30
40	68.5	18.9	1693 21 AAB48457	Human laminin 5 po
41	68.5	18.9	1693 21 AAB48459	Human laminin 5 po
42	68.5	18.9	1713 16 AAR70148	Deduced sequence o
43	68.5	18.9	1713 21 AAB48458	Human laminin 5 po
44	68.5	18.9	1724 21 AAB48456	Human laminin 5 po
45	66.5	18.4	665 22 ABB70991	Drosophila melanog

ALIGNMENTS

RESULT 1

A.318678

ID AAB18678 standard; peptide; 70 AA.

XX AAB18678;

AC AAB18678;

XX 22-JAN-2001 (first entry)

DT Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

KW ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 12 /note= "wild type residue replaced with Ala"

FT Misc-difference 13 /note= "wild type residue replaced with Ala"

FT Misc-difference 15 /note= "wild type residue replaced with Ala"

XX WO2000054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX DR WPI; 2000-618851/59.
 XX PT Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX PS Claim 53; Page 42-43; 73pp; English.
 XX CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX SQ Sequence 70 AA;
 Query Match 100.0%; Score 362; DB 21; Length 70;
 Best Local Similarity 100.0%; Pred. No. 5.6e-37;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDGAAAGCGCOTSDNDAAEALNASSKEALQIREKIPKYLFOFHNLSNL 60
 DB 1 TLVWGEFQVDGAAAGCGCOTSDNDAAEALNASSKEALQIREKIPKYLFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 2
 AAB18677
 ID AAB18677 standard; peptide; 70 AA.
 AC AAB18677;
 XX 22-JAN-2001 (first entry)
 DE Peptide fragment from Rep protein of TGMV (amino acids 110-179).
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Tomato golden mosaic virus.
 OS
 XX WO200054573-A1.
 PN 21-SEP-2000.
 PD 15-MAR-2000; 2000WO-US06759.
 PF 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX PI WPI; 2000-618851/59.
 XX DR Transgenic plants with increased resistance to geminivirus infection

XX PT Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX PS Disclosure; Page 18; 73pp; English.
 XX CC The present sequence is derived from a geminivirus replication (Rep)
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
 CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
 CC with other viral and host proteins. Mutants of the AL1 protein are used
 CC to produce transgenic plants. The mutation in AL1 is present in a
 CC ribosome binding region, and expression of mutant AL1 protein imparts
 CC increased resistance to geminivirus infection in the plant. Mutant AL1
 CC proteins are useful for producing plants having increased resistance or
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 CC beet curly top virus.
 XX SQ Sequence 70 AA;
 Query Match 96.4%; Score 349; DB 21; Length 70;
 Best Local Similarity 95.7%; Pred. No. 2.3e-35;
 Matches 67; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDGAAAGCGCOTSDNDAAEALNASSKEALQIREKIPKYLFOFHNLSNL 60
 DB 1 TLVWGEFQVDGASARGCGCOTSDNDAAEALNASSKEALQIREKIPKYLFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 3
 AAB18687
 ID AAB18687 standard; peptide; 356 AA.
 AC AAB18687;
 XX 22-JAN-2001 (first entry)
 DE Amino acid sequence of a geminivirus replication protein of TGMV.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Tomato golden mosaic virus.
 OS
 XX WO200054573-A1.
 PN 21-SEP-2000.
 PD 15-MAR-2000; 2000WO-US06759.
 PF 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX PI WPI; 2000-618851/59.
 XX DR Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX
 PS Disclosure; Page 47-48; 73pp; English.
 XX
 CC The present sequence represents a geminivirus replication (Rep)
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
 CC catalyses cleavage and ligation of single-stranded DNA, and interacts
 CC with other viral and host proteins. Mutants of the AL1 protein are used
 CC to produce transgenic plants. The mutation in AL1 is present in a
 CC ribosome binding region, and expression of mutant AL1 protein imparts
 CC increased resistance to geminivirus infection in the plant. Mutant AL1
 CC proteins are useful for producing plants having increased resistance or
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 CC beet curly top virus.
 XX
 SQ Sequence 356 AA;
 Query Match 96.4%; Score 349; DB 21; Length 356;
 Best Local Similarity 95.7%; Pred. No. 1.7e-34;
 Matches 67; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDAAGAGCGCOTSDNAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
 DB 110 TLVWGEFQVDSARGCGCOTSDNAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 169
 QY 61 DRIFDKTPEP 70
 DB 170 DRIFDKTPEP 179
 RESULT 4
 AAB18685
 ID AAB18685 standard; peptide; 70 AA.
 XX
 AC AAB18685;
 XX
 XX 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 10 /note= "wild type residue replaced with Ala"
 FT Misc-difference 20 /note= "wild type residue replaced with Ala"
 XX
 PN WO200054573-Al.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX
 DR WPI; 2000-618851/59.
 XX
 PT Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 XX
 PS Claim 53; Page 46; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 94.2%; Score 341; DB 21; Length 70;
 Best Local Similarity 94.3%; Pred. No. 2.2e-34;
 Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDAAGAGCGCOTSDNAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
 DB 1 TLVWGEFQVDSARGCGCOTSDNAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 5
 AAB18688
 ID AAB18688 standard; peptide; 70 AA.
 XX
 AC AAB18688;
 XX
 XX 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 19 /note= "wild type residue replaced with Ala"
 FT Misc-difference 20 /note= "wild type residue replaced with Ala"
 XX
 PN WO200054573-Al.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX
 DR WPI; 2000-618851/59.
 XX
 PT Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX
 PS Disclosure; Page 48; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;

Query Match 93.4%; Score 338; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 5.1e-34;
 Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGAAAGCGCQTSNDAAALNASSKEALQIIREKIPKYLFOFHNLSNL 60
 DB 1 TLVWGFQVDGARGCGCAASNDAAALNASSKEALQIIREKIPKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70

RESULT 6
 AAB18692
 ID AAB18692 standard; peptide; 70 AA.
 AC AAB18692;

22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.
 XX Tomato golden mosaic virus.

Key Location/Qualifiers
 FT Misc-difference 66 /note= "wild type residue replaced with Ala"
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"

WO200054573-A1.

21-SEP-2000.

15-MAR-2000; 2000WO-US06759.

18-MAR-1999; 99US-0125004.

09-APR-1999; 99US-0289346.

(UUNC-) UNIV NORTH CAROLINA STATE.

Hanley-Bowdoin L, Orozco BM, Kong L;

WPI; 2000-618851/59.

PT Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX
 PS Disclosure; Page 50; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;

Query Match 93.1%; Score 337; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 6.8e-34;
 Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGAAAGCGCQTSNDAAALNASSKEALQIIREKIPKYLFOFHNLSNL 60
 DB 1 TLVWGFQVDGARGCGCQTSNDAAALNASSKEALQIIREKIPKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70

RESULT 7
 AAB18684
 ID AAB18684 standard; peptide; 70 AA.
 AC AAB18684;

22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.
 XX Tomato golden mosaic virus.

Key Location/Qualifiers
 FT Misc-difference 7 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"

WO200054573-A1.

21-SEP-2000.

15-MAR-2000; 2000WO-US06759.

18-MAR-1999; 99US-0125004.

09-APR-1999; 99US-0289346.

(UUNC-) UNIV NORTH CAROLINA STATE.

Hanley-Bowdoin L, Orozco BM, Kong L;

WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX Claim 52; Page 45; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;
 SQ

Query Match 92.5%; Score 335; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 1.2e-33;
 Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLWGEFQVGGAAAGCGCTSDNDAABALNASSKEEALQIIRKIPKYLFOFHNLSNL 60
 DB 1 TLWGEAAVGGRSARGCGCTSDNDAABALNASSKEEALQIIRKIPKYLFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70

RESULT 8
 AAB18690
 ID AAB18690 standard; peptide; 70 AA.
 AC AAB18690;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 27 /note= "wild type residue replaced with Ala"
 FT Misc-difference 30 /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX

DR WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX Disclosure; Page 49; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;
 SQ

Query Match 92.5%; Score 335; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 1.2e-33;
 Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLWGEFQVGGAAAGCGCTSDNDAABALNASSKEEALQIIRKIPKYLFOFHNLSNL 60
 DB 1 TLWGEFQVGGRSARGCGCTSDNDAABALNASSKEEALQIIRKIPKYLFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70

RESULT 9
 AAB18686
 ID AAB18686 standard; peptide; 70 AA.
 AC AAB18686;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 24 /note= "wild type residue replaced with Leu"
 FT Misc-difference 25 /note= "wild type residue replaced with Leu"
 FT Misc-difference 26 /note= "wild type residue replaced with Leu"
 FT
 XX WO200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA

PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 PS Claim 52; Page 43-44; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 91.4%; Score 331; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 3.7e-33;
 Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDGAAAGCGCQTSNDAAAEALNASSKEEALQIREKIPKYLQFQHNLSNL 60
 DB 1 TLVWGFQVDGSRGCGCQTSNDAAAEALNASSKEEALQIAAIPKYLQFQHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 12
 AAB18691
 ID AAB18691 standard; peptide; 70 AA.
 XX AAB18691;
 AC AAB18691;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 34 /note= "wild type residue replaced with Ala"
 FT Misc-difference 35 /note= "wild type residue replaced with Ala"
 FT Misc-difference 36 /note= "wild type residue replaced with Ala"
 FT Misc-difference 36 /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 PN
 XX 21-SEP-2000.
 PD

XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI WPI; 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 PS Disclosure; Page 49; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 91.4%; Score 331; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 3.7e-33;
 Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDGAAAGCGCQTSNDAAAEALNASSKEEALQIREKIPKYLQFQHNLSNL 60
 DB 1 TLVWGFQVDGSRGCGCQTSNDAAAEALNASSKEEALQIREKIPKYLQFQHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 13
 AAB18681
 ID AAB18681 standard; peptide; 70 AA.
 XX AAB18681;
 AC AAB18681;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 47 /note= "wild type residue replaced with Ala"
 FT Misc-difference 48 /note= "wild type residue replaced with Ala"
 FT Misc-difference 49 /note= "wild type residue replaced with Ala"
 FT Misc-difference 49 /note= "wild type residue replaced with Ala"
 XX


```

PN WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX (UUNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT -
XX Claim 52; Page 44; 73pp; English.
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX Sequence 70 AA;
SQ Query Match 90.6%; Score 328; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 8.8e-33;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGFQVDGAAAGGCCTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
DB 1 TLVWGFQVDGSRAGGCCTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 14
AAB18683
ID AAB18683 standard; peptide; 70 AA.
XX AAB18683;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX Key Location/Qualifiers
FH Misc-difference 59
FT Misc-difference 61 /note= "wild type residue replaced with Ala"
FT Misc-difference 61 /note= "wild type residue replaced with Ala"
FT

```

```

FT Misc-difference 62 /note= "wild type residue replaced with Ala"
XX WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX (UUNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT -
XX Claim 53; Page 45; 73pp; English.
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX Sequence 70 AA;
SQ Query Match 90.3%; Score 327; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.2e-32;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGFQVDGAAAGGCCTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
DB 1 TLVWGFQVDGSRAGGCCTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 AAIFFDKTPEP 70
RESULT 15
AAB18682
ID AAB18682 standard; peptide; 70 AA.
XX AAB18682;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX Key Location/Qualifiers
FH Misc-difference 52
FT Misc-difference 52

```


FT		/note= "wild type residue replaced with Ala"
FT	Misc-difference 54	/note= "wild type residue replaced with Ala"
FT		/note= "wild type residue replaced with Ala"
FT	Misc-difference 55	/note= "wild type residue replaced with Ala"
FT		/note= "wild type residue replaced with Ala"

```

FT      /note= "wild type residue replaced with Ala"

```

FT	NAME	SEQUENCE	REMARKS
1	PROTEIN	1-100	1
2	PROTEIN	101-200	2
3	PROTEIN	201-300	3
4	PROTEIN	301-400	4
5	PROTEIN	401-500	5
6	PROTEIN	501-600	6
7	PROTEIN	601-700	7
8	PROTEIN	701-800	8
9	PROTEIN	801-900	9
10	PROTEIN	901-1000	10
11	PROTEIN	1001-1100	11
12	PROTEIN	1101-1200	12
13	PROTEIN	1201-1300	13
14	PROTEIN	1301-1400	14
15	PROTEIN	1401-1500	15
16	PROTEIN	1501-1600	16
17	PROTEIN	1601-1700	17
18	PROTEIN	1701-1800	18
19	PROTEIN	1801-1900	19
20	PROTEIN	1901-2000	20
21	PROTEIN	2001-2100	21
22	PROTEIN	2101-2200	22
23	PROTEIN	2201-2300	23
24	PROTEIN	2301-2400	24
25	PROTEIN	2401-2500	25
26	PROTEIN	2501-2600	26
27	PROTEIN	2601-2700	27
28	PROTEIN	2701-2800	28
29	PROTEIN	2801-2900	29
30	PROTEIN	2901-3000	30
31	PROTEIN	3001-3100	31
32	PROTEIN	3101-3200	32
33	PROTEIN	3201-3300	33
34	PROTEIN	3301-3400	34
35	PROTEIN	3401-3500	35
36	PROTEIN	3501-3600	36
37	PROTEIN	3601-3700	37
38	PROTEIN	3701-3800	38
39	PROTEIN	3801-3900	39
40	PROTEIN	3901-4000	40
41	PROTEIN	4001-4100	41
42	PROTEIN	4101-4200	42
43	PROTEIN	4201-4300	43
44	PROTEIN	4301-4400	44
45	PROTEIN	4401-4500	45
46	PROTEIN	4501-4600	46
47	PROTEIN	4601-4700	47
48	PROTEIN	4701-4800	48
49	PROTEIN	4801-4900	49
50	PROTEIN	4901-5000	50
51	PROTEIN	5001-5100	51
52	PROTEIN	5101-5200	52
53	PROTEIN	5201-5300	53
54	PROTEIN	5301-5400	54
55	PROTEIN	5401-5500	55
56	PROTEIN	5501-5600	56
57	PROTEIN	5601-5700	57
58	PROTEIN	5701-5800	58
59	PROTEIN	5801-5900	59
60	PROTEIN	5901-6000	60
61	PROTEIN	6001-6100	61
62	PROTEIN	6101-6200	62
63	PROTEIN	6201-6300	63
64	PROTEIN	6301-6400	64
65	PROTEIN	6401-6500	65
66	PROTEIN	6501-6600	66
67	PROTEIN	6601-6700	67
68	PROTEIN	6701-6800	68
69	PROTEIN	6801-6900	69
70	PROTEIN	6901-7000	70
71	PROTEIN	7001-7100	71
72	PROTEIN	7101-7200	72
73	PROTEIN	7201-7300	73
74	PROTEIN	7301-7400	74
75	PROTEIN	7401-7500	75
76	PROTEIN	7501-7600	76
77	PROTEIN	7601-7700	77
78	PROTEIN	7701-7800	78
79	PROTEIN	7801-7900	79
80	PROTEIN	7901-8000	80
81	PROTEIN	8001-8100	81
82	PROTEIN	8101-8200	82
83	PROTEIN	8201-8300	83
84	PROTEIN	8301-8400	84
85	PROTEIN	8401-8500	85
86	PROTEIN	8501-8600	86
87	PROTEIN	8601-8700	87

PN WO200054573-A1.

PD 21-SEP-2000.

15-MAR-2000:

PR 18-MAR-1999: 99US-0125004.

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

THE UNIVERSITY OF CHICAGO

[illegible]

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

PT comprise a nucleic acid construct containing

PT - concerning a meeting with a mission in the training region

PS Claim 53: page 44-45: 73pp: English.

CC The present sequence represents a mutant peptide, derived from a

CC geminivirus replication (rep) protein, also known as ATR. All birds
CC double-stranded DNA. catalyses cleavage and ligation of single-stranded

CC DNA, and interacts with other viral and host proteins. Mutations of the
CC protein are used to produce transgenic plants. The mutation in Al1 is

present in a ribosome binding region, and expression of mutant AAT protein imparts increased resistance to geminivirus infection in the

plasmids are useful for producing plasmids having increased resistance or reduced sensitivity to a semiovirus such as

CC tomato golden mosaic virus, tomato mullie virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian virus, tomato leaf curl virus.

CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas nemato-

CC
VIRUS, COTTON LEAF CURT VIRUS OF DEER CURRY TOP VIRUS.
XX

sequence 70 AA;

Query Match	89.88; Score 325; DB 21; Length 70;
Best Local Similarity	91.48; Pred No 2 10 22;

```
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps
```

QY I ILVWGEFQV DGRHAGGCQISNDAAAEALNASSNEBALQIREKIPKYLFFQHNTLSNL
||||| - |||||

DD I ILVWGEFQVVDGRSARGGCGTISNDAAAEALNASSKEEALQI IREK I PEKYLFFAF AALNSNL E

QY 61 DRLEUKIEP 70

DD 61 DRIFDNIEF 70

Search completed: December 23 2003 08:56:28

83225 / 9999.55 : 2000 0000

100


```

Db      110 TIWGFQVQDGRSARGGQSQSANDSYAKALNADSIESTILTKBEQPKDYVLQHHNIRSNL 169
Qy      61 DRIFDKTPEP 70
       :|||:|||
Db      170 ERIFVKVPEP 179

RESULT 2
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-46

Query Match      59.4%; Score 215; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 2.4e-19;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy      1 TLVWGFQVQDGAAGCGCOTSDNDAARALNASKEEALQIIREKIPKYLFOFHNLNSNL 60
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      110 TIWGFQVQDGRSARGGQSQSANDSYAKALNADSIESTILTKBEQPKDYVLQHHNIRSNL 169

Qy      61 DRIFDKTPEP 70
       :|||:|||
Db      170 ERIFVKVPEP 179

RESULT 3
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-46

Query Match      59.4%; Score 215; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 2.4e-19;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy      1 TLVWGFQVQDGAAGCGCOTSDNDAARALNASKEEALQIIREKIPKYLFOFHNLNSNL 60
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      110 TIWGFQVQDGRSARGGQSQSANDSYAKALNADSIESTILTKBEQPKDYVLQHHNIRSNL 169

Qy      61 DRIFDKTPEP 70
       :|||:|||
Db      170 ERIFVKVPEP 179

RESULT 4
US-08-838-151A-52
; Sequence 52, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-49

Query Match      59.4%; Score 215; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 2.4e-19;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy      1 TLVWGFQVQDGAAGCGCOTSDNDAARALNASKEEALQIIREKIPKYLFOFHNLNSNL 60
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
LJ      110 TIWGFQVQDGRSARGGQSQSANDSYAKALNADSIESTILTKBEQPKDYVLQHHNIRSNL 169

Qy      61 DRIFDKTPEP 70
       :|||:|||
Db      170 ERIFVKVPEP 179

```

```

; MOLECULE TYPE: protein
US-08-838-151A-55

Query Match          59.4%; Score 215; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 2.4e-19;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY      1 TLVGGFQVDGAAAGGCCTSDNAAAFALNASSKERALQIIRBKIPKYLQFHNLSNL 60
          :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      110 TIWGGFQVDGSRGAGGQSANDSYAKALNADIESALYILKGEQFDYVLQHNIRSNL 169
          :|||:||||:||||:||||:||||:||||:||||:||||:||||:

QY      61 DRIFDKTPEP 70
          :|||:||||
Db      170 ERIFVKVPEP 179
          :|||:||||

RESULT 6
US-08-809-103B-2
; Sequence 2, Application US/08809103B
; Patent No. 6131505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-2

Query Match 59.4%; Score 215; DB 3; Length 359;
Best Local Similarity 55.1%; Pred. No. 2.4e-19;
Matches 38; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGEFQVDGAAAGGCGTNSDAAAEALNASSKEALQITREKTPKYLQFPHNLNSLD 61
Db 111 LEWGTTFQIDGRSARGGQGTANDAYAKINAGSKSQALDVIKELAPRDYVLHFHINSLD 170
Qy 62 RIFDKTPEP 70

```

Db 171 KVFQVPPAP 179

RESULT 7

US-08-809-103B-4
 ; Sequence 4, Application US/08809103B
 ; Patent No. 6133505
 ; GENERAL INFORMATION:
 ; APPLICANT: GRONENBORN, Bruno
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS FOR OBTAINING SAME
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: YOUNG & THOMPSON
 ; STREET: 745 South 23rd Street
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/809,103B
 ; FILING DATE: 17-MAR-1997
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 94.11040
 ; FILING DATE: 15-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/FR95/01192
 ; FILING DATE: 15-SEP-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PATCH, Andrew J.
 ; REGISTRATION NUMBER: 32,925
 ; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 521-2297
 ; TELEFAX: (703) 685-0573
 ; TELEX: 248425 EMBON
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 359 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-809-103B-4

Query Match 59.4%; Score 215; DB 3; Length 359;

Best Local Similarity 55.1%; Pred. No. 2.4e-19; Indels 0; Gaps 0;
 Matches 38; Conservative 12; Mismatches 19;

QY 2 LVWGEFQVCGAAAGCQTSNDAAEALNASSKEALQIREKIPKYLQFPHNLSNLD 61
 Db 111 LEWGTFOIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFHINSNLD 170

QY 62 RIFDKTPEP 70

Db 171 KVFQVPPAP 179

RESULT 8

US-08-809-103B-6
 ; Sequence 6, Application US/08809103B
 ; Patent No. 6133505
 ; GENERAL INFORMATION:
 ; APPLICANT: GRONENBORN, Bruno
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS FOR OBTAINING SAME
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: YOUNG & THOMPSON
 STREET: 745 South 23rd Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/809,103B
 FILING DATE: 17-MAR-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 94.11040
 FILING DATE: 15-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/FR95/01192
 FILING DATE: 15-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: PATCH, Andrew J.
 REGISTRATION NUMBER: 32,925
 REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 521-2297
 TELEFAX: (703) 685-0573
 TELEX: 248425 EMBON
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-809-103B-6

Query Match 59.4%; Score 215; DB 3; Length 359;

Best Local Similarity 55.1%; Pred. No. 2.4e-19; Indels 0; Gaps 0;
 Matches 38; Conservative 12; Mismatches 19;

QY 2 LVWGEFQVCGAAAGCQTSNDAAEALNASSKEALQIREKIPKYLQFPHNLSNLD 61
 Db 111 LEWGTFOIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFHINSNLD 170

QY 62 RIFDKTPEP 70

Db 171 KVFQVPPAP 179

RESULT 9

US-08-809-103B-8
 ; Sequence 8, Application US/08809103B
 ; Patent No. 6133505
 ; GENERAL INFORMATION:
 ; APPLICANT: GRONENBORN, Bruno
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS FOR OBTAINING SAME
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: YOUNG & THOMPSON
 ; STREET: 745 South 23rd Street
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/809,103B

Tue Dec 23 09:55:22 2003

```

; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8

Query Match 59.4%; Score 215; DB 3; Length 359;
Best Local Similarity 55.1%; Pred. No. 2.4e-19;
Matches 38; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVMGFEQVDGAAAGCGCQTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 61
Db 111 LEWGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170

QY 62 RIFDKTPEP 70
Db 171 KVFQVEPPAP 179

RESULT 10
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match 58.8%; Score 213; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 4.4e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGCGCQTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 60
Db 110 TIEMGDFQIDGRSARGGQQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNSNLD 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 11
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match 58.8%; Score 213; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 4.4e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGCGCQTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 60
Db 110 TIEMGDFQIDGRSARGGQQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNSNLD 169
```

```

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 12
US-08-838-151A-6
; Sequence 6, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6

Query Match 58.8%; Score 213; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 4.4e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFQHNLSNL 60
Db 110 TIEWGDFQIDGRSARGGQQSANDSYAKALNASSVQSALAVLRREQPKDFVLQNHINRSL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 13
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8

Query Match 58.8%; Score 213; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 4.4e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFQHNLSNL 60
Db 110 TIEWGDFQIDGRSARGGQQSANDSYAKALNASSVQSALAVLRREQPKDFVLQNHINRSL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 14
US-08-838-151A-24
; Sequence 24, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8

Query Match 58.8%; Score 213; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 4.4e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFQHNLSNL 60
Db 110 TIEWGDFQIDGRSARGGQQSANDSYAKALNASSVQSALAVLRREQPKDFVLQNHINRSL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

```

```

; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8

Query Match 58.8%; Score 213; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 4.4e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFQHNLSNL 60
Db 110 TIEWGDFQIDGRSARGGQQSANDSYAKALNASSVQSALAVLRREQPKDFVLQNHINRSL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 14
US-08-838-151A-24
; Sequence 24, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8

Query Match 58.8%; Score 213; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 4.4e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFQHNLSNL 60
Db 110 TIEWGDFQIDGRSARGGQQSANDSYAKALNASSVQSALAVLRREQPKDFVLQNHINRSL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

```

```

; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-24

```

```

Query Match 55.2%; Score 200; DB 3; Length 357;
Best Local Similarity 62.3%; Pred. No. 2e-17;
Matches 38; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 4 WGEFQVDGAAAGGCGTSDNDAALNASSKBEALQIIREKIPEKYLQFHNLSNLDRI 63
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
111 FGVSIQDGRSARGGQGSANDAYAEALNSGSKSEALNLIKKEAPKDYILQFHNLSNLDRI 170
QY 64 F 64
Db 171 F 171

```

Search completed: December 23, 2003, 08:59:32
Job time : 12.6667 secs

```

RESULT 15
US-08-838-151A-27
; Sequence 27, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-27

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds

(without alignments)
172.015 Million cell updates/sec

Title: US-09-289-346B-2

Perfect score: 362

Sequence: 1 TLVWGFQVQDGAAGGCGT.....FQFHLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	362	100.0	70	10	US-09-289-346A-2
2	349	96.4	70	10	US-09-289-346A-1
3	349	96.4	356	10	US-09-289-346A-11
4	341	94.2	70	10	US-09-289-346A-9
5	338	93.4	70	10	US-09-289-346A-12
6	337	93.1	70	10	US-09-289-346A-16
7	335	92.5	70	10	US-09-289-346A-8
8	335	92.5	70	10	US-09-289-346A-14
9	334	92.3	70	10	US-09-289-346A-10
10	333	92.0	70	10	US-09-289-346A-13
11	331	91.4	70	10	US-09-289-346A-4
12	331	91.4	70	10	US-09-289-346A-15
13	328	90.6	70	10	US-09-289-346A-5
14	327	90.3	70	10	US-09-289-346A-7
15	325	89.8	70	10	US-09-289-346A-6

Sequence 3, Appli
Sequence 4, Appli
Sequence 113, Appl
Sequence 16, Appl
Sequence 4, Appli
Sequence 29, Appl
Sequence 18, Appl
Sequence 20, Appl
Sequence 50, Appl
Sequence 3, Appli
Sequence 6, Appli
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 140, Appl
Sequence 6173, Ap
Sequence 35, Appl
Sequence 10494, A
Sequence 7153, Ap
Sequence 19, Appl
Sequence 9112, Ap
Sequence 2, Appli
Sequence 244, App
Sequence 2, Appli
Sequence 20, Appl
Sequence 153, App
Sequence 153, App
Sequence 17, Appl
Sequence 5394, Ap

16 317 87.6 70 10 US-09-289-346A-3
17 69.5 19.2 512 12 US-10-301-661A-4
18 68.5 18.9 1713 15 US-10-171-311-113
19 65.5 18.1 1772 14 US-10-029-413A-16
20 65.5 18.1 2166 14 US-10-029-413A-4
21 65.5 18.1 2181 12 US-10-411-010-29
22 65.5 18.1 2181 14 US-10-029-413A-18
23 65.5 18.1 2181 14 US-10-029-413A-20
24 65.5 18.1 2181 15 US-10-205-823-50
25 65 18.0 233 15 US-10-151-336-3
26 65 18.0 335 15 US-10-151-336-6
27 62 17.1 21 10 US-09-984-056-17
28 62 17.1 21 10 US-09-984-057-17
29 62 17.1 21 12 US-10-105-232-17
30 62 17.1 21 12 US-10-189-437-17
31 62 17.1 1502 10 US-09-801-368-140
32 61 16.9 292 10 US-09-738-626-6173
33 61 16.9 712 11 US-09-893-519A-35
34 61 16.9 722 9 US-09-815-242-10494
35 61 16.9 722 12 US-10-032-585-7153
36 60 16.6 446 14 US-10-136-517-19
37 59 16.3 886 15 US-10-156-761-9112
38 58.5 16.2 299 8 US-08-831-310-2
39 58.5 16.2 299 10 US-09-881-752A-244
40 58.5 16.2 299 12 US-10-039-183A-2
41 58 16.0 844 15 US-10-179-046-20
42 57.5 15.9 266 9 US-09-791-171-153
43 57.5 15.9 266 12 US-09-804-980-153
44 57.5 15.9 535 12 US-10-205-219-17
45 57.5 15.9 643 9 US-09-815-242-5394

ALIGNMENTS

RESULT 1
US-09-289-346A-2
; Sequence 2, Application US/09289346A
; Patent No. US2002138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-jie
; APPLICANT: Grisseem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
US-09-289-346A-2

Query Match 100.0%; Score 362; DB 10; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.1e-38;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TLVWGFQVQDGAAGGCGTSDNDAALNASSKEALQIIRKIPKYLQFPHNLSNL 60
Db 1 TLVWGFQVQDGAAGGCGTSDNDAALNASSKEALQIIRKIPKYLQFPHNLSNL 60
Qy 61 DRIFDKTPEP 70

```
Db      61 DRIFDKTPEP 70
|||||
RESULT 2
US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1

Query Match      96.4%; Score 349; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 9.3e-37;
Matches 67; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 TLVWGEFQVDDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIKEPKYLFQFHNLSNL 60
|||||
Db      1 TLVWGEFQVDDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIKEPKYLFQFHNLSNL 60
|||||
QY      61 DRIFDKTPEP 70
|||||
Db      61 DRIFDKTPEP 70
|||||

RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match      96.4%; Score 349; DB 10; Length 356;
Best Local Similarity 95.7%; Pred. No. 8.1e-36;
Matches 67; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 TLVWGEFQVDDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIKEPKYLFQFHNLSNL 60
|||||
Db      1 TLVWGEFQVDDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIKEPKYLFQFHNLSNL 60
|||||
QY      61 DRIFDKTPEP 70
|||||
Db      61 DRIFDKTPEP 70
|||||

RESULT 4
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match      94.2%; Score 341; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 9.7e-36;
Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 TLVWGEFQVDDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIKEPKYLFQFHNLSNL 60
|||||
Db      1 TLVWGEFQVAGRSARGCGCQTSNDAAAEALNASSKEEALQIIRKIKEPKYLFQFHNLSNL 60
|||||
QY      61 DRIFDKTPEP 70
|||||
Db      61 DRIFDKTPEP 70
|||||

RESULT 5
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12

Query Match      93.4%; Score 338; DB 10; Length 70;
```

```
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AAl18).
US-09-289-346A-8

Query Match          92.5%; Score 335; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 5.6e-35;
Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 TLVWGEFQVDSARGGCAASNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 6
US-09-289-346A-16
; Sequence 16, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-16

Query Match          93.1%; Score 337; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 3.1e-35;
Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 7
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
```

```
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AAl18).
US-09-289-346A-8

Query Match          92.5%; Score 335; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 5.6e-35;
Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 TLVWGEAAVDGSRARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 8
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match          92.5%; Score 335; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 5.6e-35;
Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 9
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
```

```
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LLL136).
US-09-289-346A-10

Query Match          92.3%; Score 334; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 7.5e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLSNL 60
Db 1 TLVWGFQVDGSRAGCGCQTSNDLLLEALNASSKEEALQIIRKIPKYLQFPHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-13

Query Match          92.0%; Score 333; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1e-34;
Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLSNL 60
Db 1 TLVWGFQVDGSRAGCGCQTSAAAAAEALNASSKEEALQIIRKIPKYLQFPHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
```

```
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; NAME/KEY: VARIANT
; LOCATION: (42)..(44)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAA154).
US-09-289-346A-4

Query Match          91.4%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.8e-34;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLSNL 60
Db 1 TLVWGFQVDGSRAGCGCQTSNDAAAEALNASSKEEALQIAAAIPEKYLQFPHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match          91.4%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.8e-34;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLSNL 60
Db 1 TLVWGFQVDGSRAGCGCQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
```

```

RESULT 15
US-09-289-346A-6
; Sequence 6, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (52)..(55)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (QFHN165->AFAA165).
US-09-289-346A-6

Query Match          89.8%;   Score 325;   DB 10;   Length 70;
Best Local Similarity 91.4%;   Pred.No. 1e-33;
Matches 64;   Conservative 1;   Mismatches 5;   Indels 0;   Gaps 0

Qy  1  TLVWGFQVDGAAAAGCQTSNDAAAEALNASSKEBALQIIREKIPEKYLFOFHNILN
      |||||
Db   1  TLVWGFQVDGSRGARGCQTSNDAAAEALNASSKEBALQIIREKIPEKYLFAFAALN
      |||||

Qy  61  DRIFDKTTPP 70
      |||||
Db   61  DRIFDKTTPP 70
      |||||

Search completed: December 23, 2003, 09:43:28
Job time : 76 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds
(without alignments)
673.181 Million cell updates/sec

Title: US-09-289-346B-2
Perfect score: 362
Sequence: 1 TLVWGEFQVDCGAAAGGCGT.....PQHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	349	96.4	352	1 QOCVLT	Al1 protein - toma
2	249	68.8	361	1 QOCVPT	Al1 protein - toma
3	236	65.2	358	2 S07594	hypothetical prote
4	229	63.3	362	1 JQ1887	Al1 protein - toma
5	222	61.3	359	2 S39211	gene Cl protein -
6	218	60.2	349	2 JQ2300	replicase - pepper
7	218	60.2	349	2 S31875	Al1 protein - pepp
8	215	59.4	359	2 S22593	hypothetical prote
9	212	58.6	351	2 JQ2327	Al1 protein - indi
10	212	58.6	355	1 QOCVW1	AV1 protein - abut
11	209	57.7	358	1 JQ1870	Al1 protein - toma
12	209	57.7	359	2 S39235	gene Cl protein -
13	209	57.7	359	2 S28360	Al1 protein - beet
14	202	55.8	360	2 S59885	replication-associ
15	200	55.2	357	1 QOCVCI	Al1 protein - toma
16	142	39.2	131	2 S45059	Al1 protein (clone
17	124	34.3	347	1 QOCVSI	Al1 protein - squa
18	68.5	18.9	1713	2 A55347	adhesive ligand ep
19	65.5	18.1	1610	2 A46227	voltage-dependent
20	65.5	18.1	1646	2 JH0422	calcium channel al
21	65.5	18.1	2161	2 JH0564	calcium channel al
22	65.5	18.1	2181	2 A38198	voltage-dependent
23	65.5	18.1	2203	2 T42742	alcohol dehydrogen
24	65	18.0	371	2 B69502	probable peptidyl-
25	64.5	17.8	299	2 B71967	glycerol dehyde-3-p
26	64.5	17.8	335	1 DEBSGF	thiolesterase B (E
27	64.5	17.8	557	2 A47162	acetyl-CoA C-acety
28	63.5	17.5	392	2 T45290	probable NADH oxid
29	63	17.4	397	2 B71078	

MG223 homolog F10-
hypothetical prote
protein-Npi-phosph
conserved hypothet
Cl protein - tobac
UDP-glucose 4-epim
CYC1/CYP3 transcri
probable phosphoe
iron(III)-binding
acetyl-CoA C-acety
Fc gamma (Igg) rec
hypothetical prote
probable flagellar
fructose specific
E2 protein - human
CDP-diacylglycerol

30 62.5 17.3 419 2 S73846
31 62.5 17.3 1033 2 E97700
32 62 17.1 154 2 AD3475
33 62 17.1 181 2 G97976
34 62 17.1 235 2 D42452
35 62 17.1 308 2 C84072
36 62 17.1 1502 1 RBYH1
37 61.5 17.0 481 2 A70091
38 61 16.9 338 2 AG3582
39 61 16.9 392 2 T44362
40 61 16.9 587 2 JC1419
41 60.5 16.7 136 2 T22440
42 60.5 16.7 201 2 A81380
43 60.5 16.7 652 2 E89841
44 60 16.6 384 1 W2ML41
45 60 16.6 447 2 S52437

ALIGNMENTS

RESULT 1
QOCVLT
Al1 protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994
C:Accession: A04170
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
A:Residues: 1-352 <HAM>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 96.4%; Score 349; DB 1; Length 352;
Best Local Similarity 95.7%; Pred. No. 1.5e-30;
Matches 67; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDCGAAAGGCGTSDNAAALNASSKEALQIIRKIPKYLFPQHNLNSNL 60
Db 111 TLVWGEFQVDCGSRAGCGTSDNAAALNASSKEALQIIRKIPKYLFPQHNLNSNL 170

Qy 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180

RESULT 2
QOCVPT
Al1 protein - potato yellow mosaic virus (isolate Venezuela)
C:Species: potato yellow mosaic virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C:Accession: J00364
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel
A:Reference number: J00362; MUID:91311403; PMID:1856690
A:Accession: J00364
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-361 <COU>
A:Cross-references: GB:D00940; NID:g222458; PIDN:BAA00782.1; PID:g222459
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 68.8%; Score 249; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 1.4e-13;
Matches 46; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
Db 110 TLVWGFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
Qy 61 DRIFDKTPE 69
Db 170 DRIFDKTPE 178

RESULT 3
S07594
hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)
C;Species: cassava latent virus
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C;Accession: S07594
R;Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
Nucleic Acids Res. 18, 197-198, 1990
A;Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A;Reference number: S07590; MUID:90174930; PMID:2308831
A;Accession: S07594
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-358 <MOR>
A;Cross-references: EMBL:X17095; NID:959371; PIDN:CAA34953.1; PID:959376
C;Genetics:
A;Map position: segment DNAL
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 65.2%; Score 236; DB 2; Length 358;
Best Local Similarity 60.0%; Pred. No. 3.6e-18;
Matches 42; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
Db 109 TLVWGFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
Qy 61 DRIFDKTPE 70
Db 169 DRIFDKTPE 178

RESULT 4
JQ1887
AL1 protein - tomato yellow leaf curl virus (strain Australia)
N;Alternate names: CI protein
C;Species: tomato yellow leaf curl virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
C;Accession: JQ1887
R;Dry, I.B.; Rigen, J.E.; Krake, L.R.; Mullineaux, P.M.; Rezaian, M.A.
J. Gen. Virol. 74, 147-151, 1993
A;Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.
A;Reference number: JQ1885; MUID:93139778; PMID:8423446
A;Accession: JQ1887
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-362 <DRY>
A;Cross-references: GB:S53251
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 63.3%; Score 229; DB 1; Length 362;
Best Local Similarity 52.9%; Pred. No. 2.1e-17;
Matches 45; Conservative 10; Mismatches 14; Indels 16; Gaps 1;

Qy 1 TLVWGFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
Db 110 TLVWGFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
Qy 61 DRI-----FDKTP 69
|||

Db 170 DRIFDKTPE 194

RESULT 5
S39211
gene C1 protein - tomato yellow leaf curl virus
C;Species: tomato yellow leaf curl virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C;Accession: S39211
R;Noris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.
submitted to the EMBL Data Library, August 1993
A;Description: High similarity among the tomato yellow leaf curl virus isolates from tt
A;Reference number: S39209
A;Accession: S39211
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <NOR>
A;Cross-references: EMBL:Z25751; NID:9433655; PIDN:CAA81026.1; PID:9433658
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 61.3%; Score 222; DB 2; Length 359;
Best Local Similarity 58.0%; Pred. No. 1.2e-16;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 61
Db 111 LVWGFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 61
Qy 62 RIFDKTPE 70
Db 171 RIFDKTPE 179

RESULT 6
JQ2300
replicase - pepper huasteco virus (component A)
N;Alternate names: ORF AL1 protein
C;Species: pepper huasteco virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Sep-1999
C;Accession: JQ2300
R;Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estrella, L.; Rivera-Bustamante, R.
J. Gen. Virol. 74, 2225-2231, 1993
A;Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with b1
A;Reference number: JQ2299; MUID:94015007; PMID:8409944
A;Accession: JQ2300
A;Molecule type: DNA
A;Residues: 1-349 <TOR>
A;Cross-references: GB:X70418; NID:961023; PIDN:CAA49856.1; PID:961025
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 60.2%; Score 218; DB 2; Length 349;
Best Local Similarity 57.1%; Pred. No. 3.3e-16;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
Db 110 TLVWGFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
Qy 61 DRIFDKTPE 70
Db 170 NRIFDKTPE 179

RESULT 7
S31875
AL1 protein - pepper rizado amarillo virus
C;Species: pepper rizado amarillo virus
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 20-Sep-1999
C;Accession: S31875
R;Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-I
submitted to the EMBL Data Library, February 1993
A;Description: Complete nucleotide sequence of pepper huasteco virus: analysis and com
A;Reference number: S31872

A:Accession: S31875
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <TOR>
A:Cross-references: EMBL:X70418; NID:G61023; PIDN:CAA49856.1; PID:G61025
A:Note: the source is designated as pepper huasteco virus
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 60.2%; Score 218; DB 2; Length 349;
Best Local Similarity 57.1%; Pred. No. 3.3e-16;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVGGAAAGGCGTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db 110 TVEWGEFQIDGRSARGGQGSANDTYAKALNSAEALQIIRKEQFQHFLLQFHNIVNSA 169

Qy 61 DRFDKTPPEP 70
Db 170 NRIFQTPPEP 179

RESULT 8
S22593
hypothetical protein C4 - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999
C:Accession: S22593
R:Kheyr-Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.
Nucleic Acids Res. 19, 6763-6769, 1991
A:Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite virus
A:Reference number: S22598; MUID:92107660; PMID:1840676
A:Accession: S22593
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-359 <KHE>
A:Cross-references: EMBL:X61153; NID:G62211; PIDN:CAA43466.1; PID:G62217
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.4%; Score 215; DB 2; Length 359;
Best Local Similarity 55.1%; Pred. No. 7.2e-16;
Matches 38; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGEFQVGGAAAGGCGTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 61
Db 111 LEWGTQIDGRSARGGQQTANDAYAKALNAGSKQALDVIRELAPRDYVLFHFNLSNL 170

Qy 62 RIFDKTPPEP 70
Db 171 KVFQVPPAP 179

RESULT 9
JQ2327
AL1 protein - Indian cassava mosaic virus
N:Alternate names: replication-associated protein
C:Species: Indian cassava mosaic virus
C:Date: 28-Aug-1995 #sequence_revision 07-Oct-1994 #text_change 20-Sep-1999
C:Accession: JQ2327; S35883
R:Hong, Y.G.; Robinson, D.J.; Harrison, B.D.
J. Gen. Virol. 74, 2437-2443, 1993
A:Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-transmitted cassava mosaic viruses
A:Reference number: JQ2326; MUID:94065670; PMID:8245859
A:Accession: JQ2327
A:Molecule type: DNA
A:Residues: 1-351 <HON>
A:Cross-references: EMBL:Z24758; NID:G395351; PIDN:CAA80891.1; PID:G584046
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 58.6%; Score 212; DB 2; Length 351;
Best Local Similarity 59.7%; Pred. No. 1.5e-15;
Matches 40; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 4 WGEFQVGGAAAGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63
Db 113 WGTQIDGRSARGGQGSANDAYAAALNSGSKSEALKILRELAAPRDYLRDFHFISSNLDRI 172

Qy 64 FDKTPPEP 70
Db 173 FTKPPPP 179

RESULT 10
QOCVWI
AV1 protein - abutilon mosaic virus (isolate West India)
C:Species: abutilon mosaic virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Apr-1994
C:Accession: A36214
R:Frischmuth, T.; Zimmatt, G.; Jeske, H.
Virology 178, 461-468, 1990
A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as well as eukaryotic features
A:Reference number: A36214; MUID:91020984; PMID:2219703
A:Accession: A36214
A:Molecule type: DNA
A:Residues: 1-355 <FRI>
A:Cross-references: EMBL:X15983
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 58.6%; Score 212; DB 1; Length 355;
Best Local Similarity 55.7%; Pred. No. 1.5e-15;
Matches 39; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVGGAAAGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db 110 TAEWGEFQIDGRSARGGQQTANDSYAKALNAGDVQSALNILKEQPKDYVLQNHINRSNL 169

Qy 61 DRFDKTPPEP 70
Db 170 ERIFAKAPEP 179

RESULT 11
JQ1870
AL1 protein - tomato mottle virus (isolate Florida)
C:Species: tomato mottle virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
C:Accession: JQ1870
R:Abouzid, A.M.; Polston, J.E.; Hiebert, E.
J. Gen. Virol. 73, 3225-3229, 1992
A:Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated from tomato
A:Reference number: JQ1869; MUID:93107858; PMID:1469361
A:Accession: JQ1870
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <ABO>
A:Cross-references: GB:L14460
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 57.7%; Score 209; DB 1; Length 358;
Best Local Similarity 52.9%; Pred. No. 3.3e-15;
Matches 37; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVGGAAAGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db 107 TIEWGEFQIDGRSARGGQGSANDSYAKALNAGSVQSALAVUREQPKDFVLQNHINRSNL 166

Qy 61 DRFDKTPPEP 70
Db 167 ERIFAKAPEP 176

RESULT 12

S39235
gene C1 protein - tomato yellow leaf curl virus
C/Species: tomato yellow leaf curl virus
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
C/Accession: S39235
R/Crespi, S.; Noris, E.; Vaira, A.; Bosco, D.; Accotto, G.
submitted to the EMBL Data Library, December 1993
A/Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.
A/Reference number: S39233
A/Accession: S39235
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-359 <CRE>
A/Cross-references: EMBL:Z28390; NID:G1041671; PID:G1334964
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 57.7%; Score 209; DB 2; Length 359;
Best Local Similarity 53.6%; Pred. No. 3.3e-15;
Matches 37; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVMGEFQVDGAAAGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 61
Db 111 LEWTFQIDGRSARGGQQTANDAYAKAINARSKSEALDVIKQLAPRDYVLHFHNLSNLD 170

Qy 62 RIFDKTPEP 70
Db 171 KVQFVPPAP 179

RESULT 13
S28360
AL1 protein - beet curly top virus
C/Species: beet curly top virus
C/Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Sep-1999
C/Accession: S28360
R/Stanley, J.; Markham, P.G.; Callis, R.J.; Pinner, M.S.
EMBO J. 5, 1761-1767, 1986
A/Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly top
A/Reference number: S28360
A/Accession: S28360
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-385 <STA>
A/Cross-references: GB:M24597; EMBL:X04144; NID:G210678; PIDN:AAA42751.1; PID:G210679
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 57.7%; Score 209; DB 2; Length 385;
Best Local Similarity 52.9%; Pred. No. 3.5e-15;
Matches 37; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 60
Db 137 TIWGEFQIDGRSARGGQQTANDSYAKALNATSLDQALQILKEQPKDYFLQHNLSNLD 196

Qy 61 DRIFDKTPEP 70
Db 197 QKIFQRPDP 206

RESULT 14
S59885
replication-associated protein C1 - tomato yellow leaf curl virus
C/Species: tomato yellow leaf curl virus
C/Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
C/Accession: S59885
R/Hong, Y.; Harrison, B.D.
submitted to the EMBL Data Library, February 1995
A/Description: Nucleotide sequences from tomato leaf curl viruses from different countries
d geminiviruses.
A/Reference number: S58346
A/Accession: S59885
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-360 <HON>
A/Cross-references: EMBL:Z48182; NID:G944836; PIDN:CAA88229.1; PID:G974211
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 55.8%; Score 202; DB 2; Length 360;
Best Local Similarity 57.6%; Pred. No. 1.9e-14;
Matches 38; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 4 WGEFQVDGAAAGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63
Db 113 FGVSQIDGRSARGGQQTANDAYAEALNASSKEEALQIIREKAPKDFVLQFHNLSNLDRI 172

Qy 64 FDKTPE 69
Db 173 FTPSAE 178

RESULT 15
QCCVC1
AL1 protein - tomato yellow leaf curl virus
N/Alternate names: C1 protein
C/Species: tomato yellow leaf curl virus
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C/Accession: D40779
R/Navot, N.; Fichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.
Virology 185, 151-161, 1991
A/Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single
A/Reference number: A40779; MUID:92024070; PMID:1926771
A/Accession: D40779
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-357 <NAV>
A/Cross-references: GB:X15656; NID:G62204; PIDN:CAA33688.1; PID:G62207
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 55.2%; Score 200; DB 1; Length 357;
Best Local Similarity 62.3%; Pred. No. 3.1e-14;
Matches 38; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 4 WGEFQVDGAAAGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63
Db 111 FGVSQIDGRSARGGQQTANDAYAEALNASSKEEALQIIREKAPKDYILQFHNLSNLDRI 170

Qy 64 F 64
Db 171 F 171

Search completed: December 23, 2003, 09:05:17
Job time : 12 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds
(without alignments)
569.747 Million cell updates/sec

Title: US-09-289-346B-2
Perfect score: 362
Sequence: 1 TLVWGFQVQDGAAGGCQT.....FQFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	349	96.4	352	1	VAL1	TGMV	P03567 tomato gold
2	249	68.8	361	1	VAL1	PYMW	P27258 potato yell
3	236	65.2	358	1	VAL1	CLVK	P14982 cassava lat
4	236	65.2	358	1	VAL1	CLVN	P14972 cassava lat
5	229	63.3	362	1	VAL1	TYLCA	P36279 tomato yell
6	222	61.3	359	1	VAL1	TYLCU	P38609 tomato yell
7	218	60.2	349	1	VAL1	PHUV	Q06923 pepper huas
8	215	59.4	359	1	VAL1	TYLCM	P27260 tomato yell
9	213	58.8	353	1	VAL1	BGMV	P05175 bean golden
10	212	58.6	355	1	VAL1	ABMVW	P21947 abutilon mo
11	209	57.7	358	1	VAL1	ECTV	P14991 beet curly
12	209	57.7	361	1	VAL1	TMOV	Q06657 tomato mott
13	200	55.2	357	1	VAL1	TYLCV	P27259 tomato yell
14	124	34.3	347	1	VAL1	SLCV	P29048 squash leaf
15	68.5	18.9	1713	1	LM43	HUMAN	Q16787 homo sapien
16	67	18.5	298	1	OLG2	CHICK	Q080b3 gallus gall
17	65.5	18.1	1610	1	CCAD	MESAU	Q09244 mesocricetu
18	65.5	18.1	2161	1	CCAD	HUMAN	Q01668 homo sapien
19	65.5	18.1	2203	1	CCAD	RAT	P27732 rattus norv
20	64.5	17.8	299	1	Y175	HELFPJ	Q92mq7 helicobacte
21	64.5	17.8	334	1	G3P	BACST	P00362 bacillus st
22	64.5	17.8	335	1	G3P	BACCO	P15115 bacillus co
23	64.5	17.8	557	1	SASE	ANAPL	Q04791 anas platyr
24	62.5	17.3	419	1	Y223	MYCPA	P75465 mycoplasma
25	62	17.1	295	1	VAL1	TYDVA	P31617 tobacco vel
26	62	17.1	1502	1	CYP1	YEAST	P12351 saccharomyc
27	60.5	16.7	136	1	Y452	CABEL	O62250 caenorhabdi
28	60	16.6	387	1	VE2	HEV41	P27552 human papil
29	60	16.6	447	1	CDS4	DROME	P56079 d phosphati
30	60	16.6	513	1	HEMO	CHICK	P18080 gallus gall
31	59.5	16.4	863	1	AMPN	CAUCR	P37893 caulobacter
32	59	16.3	129	1	RK12	PORPU	P51339 porphyra pu
33	59	16.3	247	1	YCP4	YEAST	P25349 saccharomyc

RESULT 1
ID VAL1 TGMV STANDARD; PRT; 352 AA.
AC P03567;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
OS AC1.
GN Tomato golden mosaic virus (TGMV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10831;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;
RT *Complete nucleotide sequence of the infectious cloned DNA components
of tomato golden mosaic virus: potential coding regions and regulatory
sequences.";
RL EMBL J. 3:2197-2205(1984).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).

EMBL; K02029; -; NOT_ANNOTATED_CDS.
DR PIR; A04170; Q0CVL1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOAT1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT ATP-binding.
FT NP BIND. 223 230 ATP (POTENTIAL).
SQ SEQUENCE 352 AA; 40332 MW; C33C93859644B4A4 CRC64;

Query Match 96.4%; Score 349; DB 1; Length 352;
Best Local Similarity 95.7%; Pred. No. 2.3e-31;
Matches 67; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLVWGFQVQDGAAGGCQTSDNAAALNASSKEALQIIREKIPKYLQFQHNLSNL 60
Db 111 TLVWGFQVQDGRSARGCQTSNDAAALNASSKEALQIIREKIPKYLQFQHNLSNL 170
Qy 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180

RESULT 2
ID VAL1 PYMW STANDARD; PRT; 361 AA.
AC P27258;

```

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE All protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus.";
RL J. Gen. Virol. 72:1515-1520(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D00940; BAA00782.1; -.
DR PIR; J00364; QOCVPT.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW NP BIND. 222 229 ATP (POTENTIAL).
FT NP BIND. 361 AA; 40850 MW; 5627A33BF1264383 CRC64;
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;

Query Match 68.8%; Score 249; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 3e-20;
Matches 46; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGAAAGCGCOTSDNDAALNASSKEALQIRKIPKYLQFPHNLSNL 60
DB 110 TIEWGLFQIDGRSARGGQQTWDAABEALNAGSGTKEAAMKIKKLPKFLFYHNLSCNL 169

QY 61 DRIFDKTPE 69
DB 170 DRIFMKAPE 178

RESULT 3
VALI CLVK
ID VAL1 CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE All protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain West Kenya 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX Stanley J., Gay M.R.;
RA "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----

```

```

CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND. 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753EB92D69 CRC64;

Query Match 65.2%; Score 236; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 8.1e-19;
Matches 42; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGAAAGCGCOTSDNDAALNASSKEALQIRKIPKYLQFPHNLSNL 60
DB 109 TVEWGQFQIDGRSARGGQGSANDAYAKALNSGSKSEALNVIRLVPKDFVLQFPHNLSNL 168

QY 61 DRIFDKTPE 70
DB 169 DRIFQPPAP 178

RESULT 4
VALI CLVN
ID VAL1 CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE All protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
RL Nucleic Acids Res. 18:197-198(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X17095; CAA34953.1; -.
DR PIR; S07594; S07594.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND. 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16B80CB2D5E2C CRC64;

Query Match 65.2%; Score 236; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 8.1e-19;
Matches 42; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGAAAGCGCOTSDNDAALNASSKEALQIRKIPKYLQFPHNLSNL 60
DB 109 TVEWGQFQIDGRSARGGQGSANDAYAKALNSGSKSEALNVIRLVPKDFVLQFPHNLSNL 168

QY 61 DRIFDKTPE 70
DB 169 DRIFQPPAP 178

```

```

-----
CC EMBL; Z25751; CAA81026.1; -.
DR PIR; S39211; S39211.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3EC CRC64;

Query Match 61.3%; Score 222; DB 1; Length 359;
Best Local Similarity 58.0%; Pred. No. 2.9e-17;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVMGEFQVDGAAAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLQFHNLSNLD 61
Db 111 LEWGFQIDGRSARGGQQTANDAYAKAINAGSKSEALDVIREKAPDYILHFNHNSNLD 170
QY 62 RIFDKTPEP 70
Db 171 RVFQVPPAP 179

RESULT 7
VAL1 PHUV
ID VAL1 PHUV STANDARD; PRT; 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AL1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RT Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
RT comparison with bipartite geminiviruses.";
RL J. Gen. Virol. 74:2225-2231(1993).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X70418; CAA49856.1; -.
DR PIR; JQ2300; JQ2300.
DR PIR; S31875; S31875.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 39722 MW; D5F4E76CD56370F4 CRC64;

Query Match 60.2%; Score 218; DB 1; Length 349;
Best Local Similarity 57.1%; Pred. No. 7.9e-17;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLQFHNLSNLD 60
Db 110 TVWGEFQIDGRSARGGQQSANDYAKALNSASAEALQIREEQPHFPQFHNIVNSA 169

-----
RESULT 5
VAL1 TYLCA
ID VAL1 TYLCA STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Rigden J.E., Krake L.R., Mullineaux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
RT geminivirus.";
RL J. Gen. Virol. 74:147-151(1993).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 63.3%; Score 229; DB 1; Length 362;
Best Local Similarity 52.9%; Pred. No. 4.9e-18;
Matches 45; Conservative 10; Mismatches 14; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDGAAAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLQFHNLSNLD 60
Db 110 TLEWGEFQIDGRSARGGQQSANDYAKALNTGSKSEALNVRELAPDYILQFHNLSNLD 169
QY 61 DRI-----FKTPE 69
Db 170 DRIPTPLEVYVSPFLSSSPDRVPE 194

RESULT 6
VAL1 TYLCU
ID VAL1 TYLCU STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Noris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
RT from the west Mediterranean basin: the nucleotide sequence of an
RT infectious clone from Spain.";
RL Arch. Virol. 135:165-170(1994).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

```
QY 61 DRIFDKTPEP 70
Db 170 NRIFQTPPEP 179

RESULT 8
ID VAL1 TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92107660; PubMed=1840676;
RA Kheyt-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a
RT whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M10070; AAA46318.1; --
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
CC NP BIND 222 229 ATP (POTENTIAL).
CC SEQUENCE 359 AA; 40733 MW; 9717B407C93EFA7 CRC64;
Query Match 59.4%; Score 215; DB 1; Length 359;
Best Local Similarity 55.1%; Pred. No. 1.7e-16;
Matches 38; Conservative 12; Mismatches 19; Indels 0; Gaps 0;
QY 2 LVWGEFQVGGAAAGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 61
Db 111 LEMGTFTQIDGRSARGGQGTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNINSNLD 170
QY 62 RIFDKTPEP 70
Db 171 KVFQVPEP 179

RESULT 9
ID VAL1 BGMV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE AL1 protein (40.2 kDa protein).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimrat G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X15983; --; NOT ANNOTATED_CDS.
CC PIR; A36214; QOCVW1.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
QY 1 TLVWGEFQVGGAAAGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 60
Db 110 TIEMGFQVDRGSRGQGSANDSYAKALNADSIESTILKEEQPDYVQLQHNIRSNL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFKVPPEP 179

RESULT 10
ID VAL1 ABMVW STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimrat G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X15983; --; NOT ANNOTATED_CDS.
CC PIR; A36214; QOCVW1.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
QY 1 TLVWGEFQVGGAAAGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 60
Db 110 TIEMGFQVDRGSRGQGSANDSYAKALNADSIESTILKEEQPDYVQLQHNIRSNL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFKVPPEP 179

Query Match 58.8%; Score 213; DB 1; Length 353;
Best Local Similarity 57.1%; Pred. No. 2.9e-16;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;
QY 1 TLVWGEFQVGGAAAGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 60
Db 110 TIEMGFQVDRGSRGQGSANDSYAKALNADSIESTILKEEQPDYVQLQHNIRSNL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFKVPPEP 179
```

```

FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 355 AA; 40257 MW; 16A2CA8AG3251E95 CRC64;

Query Match 58.6%; Score 212; DB 1; Length 355;
Best Local Similarity 55.7%; Pred. No. 3.7e-16;
Matches 39; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGTSDNDAARALNASSKEEALQIREKIPKYLQFPHNLNSNL 60
Db 110 TLVWGEFQVDGAAAGGCGTSDNDAARALNASSKEEALQIREKIPKYLQFPHNLNSNL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 11
VAL1_BCTV STANDARD; PRT; 358 AA.
AC P14991;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
RT beet curly top virus."
RL EMBO J. 5:1761-1767 (1986).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X04144; -; NOT_ANNOTATED_CDS.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
CC FT NP_BIND 222 229 ATP (POTENTIAL).
CC SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match 57.7%; Score 209; DB 1; Length 358;
Best Local Similarity 52.9%; Pred. No. 8.1e-16;
Matches 37; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGTSDNDAARALNASSKEEALQIREKIPKYLQFPHNLNSNL 60
Db 110 TLVWGEFQVDGAAAGGCGTSDNDAARALNASSKEEALQIREKIPKYLQFPHNLNSNL 169

QY 61 DRIFDKTPEP 70
Db 170 QKIFRPPDP 179

RESULT 12
VAL1_TM0V STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.

```

```

GN AL1.
OS Tomato mottle virus (isolate Florida) (TMov).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93107858; PubMed=1469361;
RA Abouzid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida."
RL J. Gen. Virol. 73:3225-3229 (1992).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L14460; AAC32414.1; -
CC PIR; JQ1870; JQ1870.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
CC KW NP_BIND 222 229 ATP (BY SIMILARITY).
CC SEQUENCE 361 AA; 40516 MW; 8138B65CEAC6950 CRC64;

Query Match 57.7%; Score 209; DB 1; Length 361;
Best Local Similarity 52.9%; Pred. No. 8.1e-16;
Matches 37; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGTSDNDAARALNASSKEEALQIREKIPKYLQFPHNLNSNL 60
Db 110 TLVWGEFQVDGAAAGGCGTSDNDAARALNASSKEEALQIREKIPKYLQFPHNLNSNL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 13
VAL1_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (Cl protein).
GN Cl.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94024070; PubMed=1926771;
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component."
RL Virology 185:151-161 (1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

```

DR EMBL; X15656; CAA33688.1; -.
DR PIR; D40779; QQCVC1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1.1.
KW ATP-binding.
FT NP BIND 219 226 ATP (POTENTIAL).
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match
Best Local Similarity 62.3%; Pred. No. 8e-15;
Matches 38; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 4 WGEFQVDAAGCGQTSNDAAAEALNASSKEALQIIRKIPKYLQFQHNLSNLDRI 63
Db 111 FGVSDIGSRGQQSQANDAYAEALNSGSKSEALNLIKAPKDYILQFHNLSNLDRI 170

Qy 64 F 64
Db 171 F 171

RESULT 14
VAL1 SLCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE A11 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9108249; PubMed=1984668;
RA Lazarowitz S.G., Lazdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype.";
RL Virology 180:58-69(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M38183; AAC32410.1; ALT_INIT.
DR PIR; C36785; QQCVS1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1.1.
KW ATP-binding.
FT NP BIND 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDABEDDE122110E CRC64;

Query Match
Best Local Similarity 34.3%; Score 124; DB 1; Length 347;
Matches 25; Conservative 14; Mismatches 23; Indels 4; Gaps 1;

Qy 5 GEFQVDAAGCGQTSNDAAAEALNASSKEALQIIRKIPKYLQFQHNLSNLDRI 64
Db 116 GQYKVGSG---GSKSNKDDVYHNAVAGSAGEALDIKAGDPKTFIVYHNLNANVERLF 171

Qy 65 DKTPPEP 70
Db 172 QKPEP 177

```

```

RESULT 15
LMA3 HUMAN STANDARD; PRT; 1713 AA.
ID LMA3 HUMAN
AC O16787; Q13679; Q13680;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Laminin alpha-3 chain precursor (Epiligrin 170 kDa subunit) (E170)
DE (Nuclein alpha subunit).
DE LAMA3.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Keratinocytes;
RX MEDLINE=94357926; PubMed=8077230;
RA Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
RT "Cloning of the LAMA3 gene encoding the alpha 3 chain of the adhesive
RT ligand epiligrin. Expression in wound repair.";
RL J. Biol. Chem. 269:22779-22787(1994).
RN [2]
RP SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=96163880; PubMed=8586427;
RA Vidal F., Baudoin C., Miquel C., Galliano M.-F., Christiano A.M.,
RA Utito J., Ortonne J.-P., Meneguzzi G.;
RT "Cloning of the laminin alpha 3 chain gene (LAMA3) and identification
RT of a homozygous deletion in a patient with Herlitz junctional
RT epidermolysis bullosa.";
RL Genomics 30:273-280(1995).
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -1- FUNCTION: LAMININ-5 IS THOUGHT TO BE INVOLVED IN (1) CELL ADHESION
CC VIA INTEGRIN ALPHA-3/BETA-1 IN FOCAL ADHESION AND INTEGRIN ALPHA-
CC 6/BETA-4 IN HEMIDESMOSOMES, (2) SIGNAL TRANSDUCTION VIA TYROSINE
CC PHOSPHORYLATION OF P125-FAK AND P80, (3) DIFFERENTIATION OF
CC KERATINOCYTES.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The alpha-3 chain is a subunit of laminin-5
CC (epiligrin/kalinin/nicein), and possibly also a component of
CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC MEMBRANES (MAJOR COMPONENT).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=Q16787-1; Sequence=Displayed;
CC Name=B;
CC IsoId=Q16787-2; Sequence=VSP_003037;
CC Note=Sequence incomplete;
CC -1- TISSUE SPECIFICITY: SKIN; RESPIRATORY, URINARY, AND DIGESTIVE
CC EPITHELIA AND IN OTHER SPECIALIZED TISSUES WITH PROMINENT
CC SECRETORY OR PROTECTIVE FUNCTIONS. EPITHELIAL BASEMENT MEMBRANE,
CC AND EPITHELIAL CELL TONGUE THAT MIGRATES INTO A WOUND BED. A
CC DIFFERENTIAL AND FOCAL EXPRESSION OF THE ALPHA-3 CHAIN IS OBSERVED
CC IN THE CNS.
CC -1- INDUCTION: LAMININ-5 IS UP-REGULATED IN WOUND SITES OF HUMAN SKIN.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAIN G IS GLOBULAR.
CC -1- DISEASE: DEFECTS IN LAMA3 ARE A CAUSE OF JUNCTIONAL EPIDERMOLYSIS
CC BULLOSA (JEB) GRAVIS, ALSO KNOWN AS HERLITZ TYPE JEB. IT IS A
CC BLISTERING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION
CC OF BASAL CELLS FROM THE BASEMENT MEMBRANE DUE TO A DECREASED
CC NUMBER OF HEMIDESMOSOMES. LAMININ-5 IS MISSING FROM THE BASEMENT

```

MEMBRANE OF PATIENTS WITH THE GRAVIS FORM OF EPIDERMOLYSIS BULLOSA.

-!- SIMILARITY: Contains 3 laminin EGF-like domains.

-!- SIMILARITY: Contains 5 laminin G-like domains.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; L34155; AAAS9483.1; -

EMBL; X85107; CAA59428.1; -

EMBL; X85108; CAA59429.1; -

PIR; A55347; A55347.

HSSP; P02468; ITRF.

Genew; HGNC:6483; LAMA3.

MIM; 600805; -

MIM; 226700; -

GO; GO:0003604; C:basement membrane; TAS.

GO; GO:0008544; P:epidermal differentiation; TAS.

InterPro; IPR006209; EGF like.

InterPro; IPR002049; Laminin EGF.

InterPro; IPR001791; Laminin G.

Pfam; PF00053; laminin_EGF; 2.

SMART; SM00054; laminin_G; 2.

SMART; SM00180; EGF_Lam; 2.

SMART; SM00282; LamG; 5.

PROSITE; PS00022; EGF 1; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01248; LAMININ TYPE EGF; 2.

PROSITE; PS50025; LAM_G DOMAIN; 5.

Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Alternative splicing; Epidermolysis bullosa.

FT SIGNAL 1 20 POTENTIAL

FT CHAIN 21 1713 LAMININ ALPHA-3 CHAIN.

FT DOMAIN 46 201 DOMAIN III A.

FT DOMAIN 67 113 LAMININ EGF-LIKE 1.

FT DOMAIN 114 166 LAMININ EGF-LIKE 2.

FT DOMAIN 167 185 LAMININ EGF-LIKE 3 (INCOMPLETE).

FT DOMAIN 186 769 DOMAIN II AND I.

FT DOMAIN 770 971 LAMININ G-LIKE 1.

FT DOMAIN 978 1140 LAMININ G-LIKE 2.

FT DOMAIN 1147 1307 LAMININ G-LIKE 3.

FT DOMAIN 1366 1530 LAMININ G-LIKE 4.

FT DOMAIN 1537 1710 LAMININ G-LIKE 5.

FT DOMAIN 231 327 COILED COIL (POTENTIAL).

FT DOMAIN 396 548 COILED COIL (POTENTIAL).

FT DOMAIN 594 621 COILED COIL (POTENTIAL).

FT DOMAIN 702 785 COILED COIL (POTENTIAL).

FT DOMAIN 1686 1713 COILED COIL (POTENTIAL).

FT DISULFID 67 76 BY SIMILARITY.

FT DISULFID 69 83 BY SIMILARITY.

FT DISULFID 86 95 BY SIMILARITY.

FT DISULFID 98 111 BY SIMILARITY.

FT DISULFID 114 126 BY SIMILARITY.

FT DISULFID 116 135 BY SIMILARITY.

FT DISULFID 137 146 BY SIMILARITY.

FT DISULFID 149 164 BY SIMILARITY.

FT DISULFID 202 202 INTERCHAIN (PROBABLE).

FT DISULFID 205 205 INTERCHAIN (PROBABLE).

FT SITE 658 660 CELL ATTACHMENT SITE (POTENTIAL).

FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 645 645 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 882 882 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 964 964 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1108 1108 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1131 1131 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1325 1325 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1477 1477 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1667 1667 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPLIC 1 45 MGLWTFGAALGQCLGYSSQQQRVPFLQPPGSQLQASYVE

FT FRPS -> KVSSTGYGLTYQAQSFALPGDWLLEKPDVQL

FT TQCHMSIIYEETNTPRDLRHGRVHVVEGNFRHASSRAPV

FT SREELMTVLSRLADVRIQGLYPTETQRLTLSEVGLREASDT

FT GSGRIALAVEICACPPAYAGDSC (in isoform B).

FT /FTID=VSP 003037.

FT W -> R (IN REF. 2).

FT CONFLICT 123 125

FT CONFLICT 481 481

FT CONFLICT 754 754

FT CONFLICT 969 969

FT CONFLICT 1052 1052

FT CONFLICT 1184 1184

FT CONFLICT G -> A (IN REF. 2).

SQ SEQUENCE 1713 AA; 189304 MW; 45EA9BE1017B60D3 CRC64;

Query Match 18.9%; Score 68.5; DB 1; Length 1713;

Best Local Similarity 36.1%; Pred.No.18;

Matches 22; Conservative 11; Mismatches 21; Indels 7; Gaps 3;

QY 9 VDGAAAGCGCQTSNDAAAEALN--ASSKEEALQ-IIREKIPKYLQFHHNLNSNLDRIFD 65

Db 553 VDAATAYENILNAIKAEADAANRAASASSEALQTVIKEDLPK-----AKTLSSNSDKLLN 608

QY 66 K 66

Db 609 E 609

Search completed: December 23, 2003, 08:57:35

Job time : 7.77778 secs

SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;

Query Match 77.6%; Score 281; DB 12; Length 226;
 Best Local Similarity 77.1%; Pred. No. 1.1e-23;
 Matches 54; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDCGAAAGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 60
 Db 111 TLVWGEFQVDCGAAAGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 170

Qy 61 DRIFDKTPEP 70
 Db 171 DRIFAKAPEP 180

RESULT 6

Q67574 PRELIMINARY; PRT; 361 AA.

AC Q67574;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Putative replicative protein.
 GN ALI.
 OS Bean Golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10839;

RP SEQUENCE FROM N.A.
 RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
 RA Maxwell D.P., Russell D.R.;
 RA "Cloning of the complete DNA genomes of four bean-infecting
 RT geminiviruses and determining their infectivity by electric discharge
 RT particle acceleration.";
 RL Phytopathology 81:980-985(1991).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
 RA Morales F.J., Maxwell D.P.;
 RA "Differentiation of bean-infecting geminiviruses by nucleic acid
 RT hybridization probes and aspects of bean golden mosaic in Brazil.";
 RL Plant Dis. 75:336-342(1991).
 RN [3]

RP SEQUENCE FROM N.A.
 RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
 RA "Genetic diversity in geminiviruses causing bean golden mosaic
 RT disease: The nucleotide sequence of the infectious cloned DNA
 RT components of a Brazilian isolate of bean golden mosaic geminivirus.";
 RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M88686; AAA46312.1; -.
 DR InterPro; IPR001191; Geminivirus.
 DR Pfam; PF00799; Geminivirus.
 DR PRINTS; PR00227; GEMCOATALL.
 DR PRODOM; PD000736; Geminivirus.
 DR PRODOM; PD000736; Geminivirus.
 SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 77.1%; Score 279; DB 12; Length 361;
 Best Local Similarity 76.1%; Pred. No. 3.3e-23;
 Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 4 WGEFQVDCGAAAGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63
 Db 113 WGEFQVDCGAAAGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 172

Qy 64 FDKTPEP 70
 Db 173 FTKAPDP 179

RESULT 7

Q9QDB1 PRELIMINARY; PRT; 225 AA.

AC Q9QDB1;

DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Replication associated protein (Fragment).
 GN REP.
 OS Cowpea golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=69263;
 RP SEQUENCE FROM N.A.
 RA Faria J.C.;
 RA "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
 RT Brazil.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF188708; AAF06318.1; -.
 DR InterPro; IPR001191; Geminivirus.
 DR Pfam; PF00799; Geminivirus.
 DR PRINTS; PR00227; GEMCOATALL.
 DR PRODOM; PD000736; Geminivirus.
 DR PRODOM; PD000736; Geminivirus.
 FT NON TER 225 225
 SQ SEQUENCE 225 AA; 25766 MW; 1089CB6BD8D15B5D CRC64;

Query Match 76.5%; Score 277; DB 12; Length 225;
 Best Local Similarity 76.1%; Pred. No. 3.1e-23;
 Matches 51; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 4 WGEFQVDCGAAAGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63
 Db 113 WGEFQVDCGAAAGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 172

Qy 64 FDKTPEP 70
 Db 173 FTKPPEP 179

RESULT 8

Q9ELT8 PRELIMINARY; PRT; 314 AA.

AC Q9ELT8;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Replication associated protein.
 GN ACI.
 OS Sweet potato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=100755;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
 RA "Detection of a geminivirus infecting sweet potato in the United
 RT States.";
 RL Plant Dis. 82:1253-1257(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF288227; AAG01006.1; -.
 DR InterPro; IPR001191; Geminivirus.
 DR Pfam; PF00799; Geminivirus.
 DR PRINTS; PR00227; GEMCOATALL.
 DR PRODOM; PD000736; Geminivirus.
 DR PRODOM; PD000736; Geminivirus.
 SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 76.5%; Score 277; DB 12; Length 314;
 Best Local Similarity 79.4%; Pred. No. 4.6e-23;
 Matches 54; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDCGAAAGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 60
 Db 110 TLVWGEFQVDCGAAAGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 169

```

QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 9
Q9QS55 PRELIMINARY; PRT; 364 AA.
AC Q9QS55;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RL States.";
RL Plant Dis. 82:1253-1257 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RT virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0 (1999).
DR EMBL; AF104036; A047173.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 76.5%; Score 277; DB 12; Length 364;
Best Local Similarity 79.4%; Pred. No. 5.5e-23;
Matches 54; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGAAAGCGCOTSDAAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
Db 110 TIWGFQIDGRSARGGQQTANDAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 169
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica;
RA Roye M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed
RT species Sida spp. Macroptilium lathyroides, and Wissadula amplissima
RT from Jamaica.";
RL Plant Dis. 81:1251-1258 (1997).
DR EMBL; U67926; AAB97865.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.

QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 11
Q8QPU4 PRELIMINARY; PRT; 235 AA.
AC Q8QPU4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (fragment).
GN AC1.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=MG-B11;
RA Ribeiro S.G., Ambrozovicius L.P., de Avila A.C., Calegario R.F.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049208; AAL82833.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BE0DD9C810 CRC64;

Query Match 74.6%; Score 270; DB 12; Length 235;
Best Local Similarity 73.1%; Pred. No. 2e-22;
Matches 49; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 4 WGEFQVDGAAAGCGCOTSDAAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 63
Db 113 WGFQIDGRSARGGQQTANDAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 172
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 64 DRIFDKTP 70
Db 173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

```

```
RT "Characterization and genetic diversity of PYMV from the Caribbean.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY126611; AAM95995.1; -  
DR InterPro; IPR001191; Gemini_AL1.  
DR Pfam; PF00799; Gemini_AL1; 1.  
DR PRINTS; PR00227; GEMCOATALL.  
DR ProDom; PD000736; Gemini_AL1; 1.  
FT NON_TER 208 208  
SQ SEQUENCE 208 AA; 23667 MW; 51211D58FAD690A6 CRC64;  
  
Query Match 74.3%; Score 269; DB 12; Length 208;  
Best Local Similarity 70.0%; Pred. No. 2.3e-22;  
Matches 49; Conservative 13; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 TLVWGEFQVDAAGAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 60  
Db 110 TIEMGFQIDGRSARGGQOTSNDAAAEALNSGKEAMKIIKEKLPKFLFOYHNLSSNL 169  
  
Qy 61 DRIFDKTPEP 70  
Db 170 DRIFWKAPKP 179  
  
RESULT 13  
Q8JLY5 PRELIMINARY; PRT; 289 AA.  
AC Q8JLY5;  
DT 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE Replication-associated protein (Fragment).  
GN AC1.  
OS Potato yellow mosaic virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI_TaxID=10827;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;  
RT "Characterization and genetic diversity of PYMV from the Caribbean.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY126610; AAM95993.1; -  
DR InterPro; IPR001191; Gemini_AL1.  
DR Pfam; PF00799; Gemini_AL1; 1.  
DR PRINTS; PR00227; GEMCOATALL.  
DR ProDom; PD000736; Gemini_AL1; 1.  
FT NON_TER 289 289  
SQ SEQUENCE 289 AA; 32971 MW; 4ECF52F4C69C6764 CRC64;  
  
Query Match 74.3%; Score 269; DB 12; Length 289;  
Best Local Similarity 70.0%; Pred. No. 3.4e-22;  
Matches 49; Conservative 13; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 TLVWGEFQVDAAGAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 60  
Db 110 TIEMGFQIDGRSARGGQOTSNDAAAEALNSGKEAMKIIKEKLPKFLFOYHNLSSNL 169  
  
Qy 61 DRIFDKTPEP 70  
Db 170 DRIFWKAPKP 179  
  
RESULT 14  
P88975 PRELIMINARY; PRT; 149 AA.  
AC P88975;  
DT 01-MAY-1997 (TremBLrel. 03, Created)  
DT 01-MAY-1997 (TremBLrel. 03, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE Replication-associated protein (Fragment).  
GN AC1.  
OS Macroptilium golden mosaic virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI_TaxID=51676;
```

```
RN SEQUENCE FROM N.A.  
RP STRAIN=Jamaican;  
RA Roye M.E.;  
RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.  
DR EMBL; U75278; AAB36919.1; -  
DR InterPro; IPR001191; Gemini_AL1.  
DR Pfam; PF00799; Gemini_AL1; 1.  
DR PRINTS; PR00227; GEMCOATALL.  
DR ProDom; PD000736; Gemini_AL1; 1.  
FT NON_TER 149 149  
SQ SEQUENCE 149 AA; 16785 MW; E4CF5ED4C9CD508 CRC64;  
  
Query Match 73.5%; Score 266; DB 12; Length 149;  
Best Local Similarity 68.6%; Pred. No. 3.3e-22;  
Matches 48; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
  
Qy 1 TLVWGEFQVDAAGAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 60  
Db 52 TIEMGFQIDGRSARGGQOTSNDAAAEALNSGKEAMRIVKEKLPKFLFOYHNLSSNL 111  
  
Qy 61 DRIFDKTPEP 70  
Db 112 DRIFWKDPEP 121  
  
RESULT 15  
Q9YLA4 PRELIMINARY; PRT; 233 AA.  
AC Q9YLA4;  
DT 01-MAY-1999 (TremBLrel. 10, Created)  
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE Replication associated protein (Fragment).  
GN REP.  
OS Macroptilium golden mosaic virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI_TaxID=51676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Jamaica strain 1;  
RA Roye M.E.;  
RT "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica.";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Jamaica strain 1;  
RA Roye M.E., McLaughlin W.A., Maxwell D.P.;  
RT "Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica.";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF098940; AAD17850.1; -  
DR InterPro; IPR001191; Gemini_AL1.  
DR Pfam; PF00799; Gemini_AL1; 1.  
DR PRINTS; PR00227; GEMCOATALL.  
DR ProDom; PD000736; Gemini_AL1; 1.  
FT NON_TER 233 233  
SQ SEQUENCE 233 AA; 26356 MW; AA490AF4D2166A02 CRC64;  
  
Query Match 73.5%; Score 266; DB 12; Length 233;  
Best Local Similarity 68.6%; Pred. No. 5.7e-22;  
Matches 48; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
  
Qy 1 TLVWGEFQVDAAGAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 60  
Db 110 TIEMGFQIDGRSARGGQOTSNDAAAEALNSGKEAMRIVKEKLPKFLFOYHNLSSNL 169  
  
Qy 61 DRIFDKTPEP 70  
Db 170 DRIFWKDPEP 179
```

Search completed: December 23, 2003, 09:03:34
Job time : 27.3333 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	358	100.0	70	21	AA18679
2	347	96.9	70	21	AA18691
3	343	95.8	70	21	AA18690
4	332	92.7	70	21	AA18677
5	332	92.7	356	21	AA18687
6	324	90.5	70	21	AA18685
7	321	89.7	70	21	AA18688
8	320	89.4	70	21	AA18692
9	318	88.8	70	21	AA18684

XX
PD 21-SEP-2000.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

```

PF 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX PA
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX PI
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
XX Claim 52; Page 43; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 100.0%; Score 358; DB 21; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 5.8e-39;
XX Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TLVWGFQVQDGRSARGCGCQTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
DB 1 TLVWGFQVQDGRSARGCGCQTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
XX
RESULT 2
AAB18691
XX AC AAB18691 standard; peptide; 70 AA.
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Key Misc-difference 34 /note= "wild type residue replaced with Ala"
XX FT
XX Key Misc-difference 35 /note= "wild type residue replaced with Ala"
XX FT
XX Key Misc-difference 36 /note= "wild type residue replaced with Ala"
XX FT
XX Key Misc-difference 37 /note= "wild type residue replaced with Ala"
XX FT
XX WO200054573-A1.

```

```

XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX PA
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX PI
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
XX Disclosure; Page 49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 96.9%; Score 347; DB 21; Length 70;
XX Best Local Similarity 97.1%; Pred. No. 1.6e-37;
XX Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 TLVWGFQVQDGRSARGCGCQTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
DB 1 TLVWGFQVQDGRSARGCGCQTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
XX
RESULT 3
AAB18690
XX ID AAB18690 standard; peptide; 70 AA.
XX
XX AC AAB18690;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Key Misc-difference 27 /note= "wild type residue replaced with Ala"
XX FT
XX Key Misc-difference 30 /note= "wild type residue replaced with Ala"
XX FT
XX Key Misc-difference 31 /note= "wild type residue replaced with Ala"
XX FT
XX WO200054573-A1.

```



```

XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX
XX
XX Disclosure; Page 47-48; 73pp; English.
XX
XX The present sequence represents a geminivirus replication (Rep)
XX protein, which is also known as AL1. AL1 binds double-stranded DNA,
XX catalyzes cleavage and ligation of single-stranded DNA, and interacts
XX with other viral and host proteins. Mutants of the AL1 protein are used
XX to produce transgenic plants. The mutation in AL1 is present in a
XX ribosome binding region, and expression of mutant AL1 protein imparts
XX increased resistance to geminivirus infection in the plant. Mutant AL1
XX proteins are useful for producing plants having increased resistance or
XX reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
XX tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
XX virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
XX yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
XX squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
XX beet curly top virus.
XX
XX
XX Sequence 356 AA;
XX
XX Query Match 92.7%; Score 332; DB 21; Length 356;
XX Best Local Similarity 92.9%; Pred. No. 1.1e-34;
XX Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 TLVWGFEVDGRSGCGCQTSNDAAAALAAASGAALQIIRKIPKYLQFPHNLNSNL 60
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX Db 110 TLVWGFEVDGRSGCGCQTSNDAAAALAAASGAALQIIRKIPKYLQFPHNLNSNL 169
XX
XX QY 61 DRIFDKTPEP 70
XX |||||||||||
XX Db 170 DRIFDKTPEP 179
XX
XX RESULT 6
XX AAB18685
XX ID AAB18685 standard; peptide; 70 AA.
XX
XX AC AAB18685;
XX
XX DT 22-JAN-2001 (first entry)
XX
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX
XX PH Key Location/Qualifiers
XX FT Misc-difference 10 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 20 /note= "wild type residue replaced with Ala"
XX
XX PN WO200054573-A1.
XX
XX PD 21-SEP-2000.
XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX

```

```

PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX
XX
XX Claim 53; Page 46; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX
XX Sequence 70 AA;
XX
XX Query Match 90.5%; Score 324; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 1.6e-34;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 TLVWGFEVDGRSGCGCQTSNDAAAALAAASGAALQIIRKIPKYLQFPHNLNSNL 60
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX Db 1 TLVWGFEVDGRSGCGCQTSNDAAAALAAASGAALQIIRKIPKYLQFPHNLNSNL 60
XX
XX QY 61 DRIFDKTPEP 70
XX |||||||||||
XX Db 61 DRIFDKTPEP 70
XX
XX RESULT 7
XX AAB18688
XX ID AAB18688 standard; peptide; 70 AA.
XX
XX AC AAB18688;
XX
XX DT 22-JAN-2001 (first entry)
XX
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX
XX PH Key Location/Qualifiers
XX FT Misc-difference 19 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 20 /note= "wild type residue replaced with Ala"
XX
XX PN WO200054573-A1.
XX
XX PD 21-SEP-2000.
XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX

```

XX (UYN(-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX
 XX Disclosure; Page 48; 73pp; English.
 XX
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA;
 SQ
 Query Match 89.7%; Score 321; DB 21; Length 70;
 Best Local Similarity 90.0%; Pred. No. 3.9e-34;
 Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDRSGRGCGQTSNDAAAALASSAAALQIREKIPEKYLQFHNLSNL 60
 DB 1 TLVWGEFQVDRSGRGCGQTSNDAAAALASSAAALQIREKIPEKYLQFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 8
 AAB18692
 ID AAB18692 standard; peptide; 70 AA.
 AC AAB18692;
 DT 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 KW
 XX Synthetic.
 OS Tomato Golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 66 /note= "wild type residue replaced with Ala"
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR

PR 09-APR-1999; 99US-0289346.
 XX (UYN(-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX
 XX Disclosure; Page 50; 73pp; English.
 XX
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA;
 SQ
 Query Match 89.4%; Score 320; DB 21; Length 70;
 Best Local Similarity 90.0%; Pred. No. 5.3e-34;
 Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDRSGRGCGQTSNDAAAALASSAAALQIREKIPEKYLQFHNLSNL 60
 DB 1 TLVWGEFQVDRSGRGCGQTSNDAAAALASSAAALQIREKIPEKYLQFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 9
 AAB18684
 ID AAB18684 standard; peptide; 70 AA.
 AC AAB18684;
 DT 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 KW
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 7 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX

```

PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 52; Page 45; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
SQ
Query Match 88.8%; Score 318; DB 21; Length 70;
Best Local Similarity 90.0%; Pred. No. 9.7e-34;
Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 TLVWGFQVDRSGCGCQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 60
Db 1 TLVWGEAVDGRSARGCGCQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 10
AAB18678
ID AAB18678 standard; peptide; 70 AA.
XX
AC AAB18678;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 12 /note= "wild type residue replaced with Ala"
FT Misc-difference 13 /note= "wild type residue replaced with Ala"
FT Misc-difference 15 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX
15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 53; Page 42-43; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
SQ
Query Match 88.5%; Score 317; DB 21; Length 70;
Best Local Similarity 88.6%; Pred. No. 1.3e-33;
Matches 62; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
Qy 1 TLVWGFQVDRSGCGCQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 60
Db 1 TLVWGEAVDGRSARGCGCQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 11
AAB18686
ID AAB18686 standard; peptide; 70 AA.
XX
AC AAB18686;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 24 /note= "wild type residue replaced with Leu"
FT Misc-difference 25 /note= "wild type residue replaced with Leu"
FT Misc-difference 26 /note= "wild type residue replaced with Leu"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX

```

PN WO200054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX PA
 XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX DR WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX Claim 53; Page 46; 73pp; English.
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA;
 SQ Query Match 88.5%; Score 317; DB 21; Length 70;
 Best Local Similarity 88.6%; Pred. No. 1.3e-33;
 Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIEKIPKYLFOFHNLSNL 60
 Db 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEALQIIEKIPKYLFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 Db 61 DRIFDKTPEP 70
 XX RESULT 12
 AAB18689
 ID AAB18689 standard; peptide; 70 AA.
 XX AC AAB18689;
 XX 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 FH Misc-difference 22
 FT /note= "wild type residue replaced with Ala"
 FT Misc-difference 23
 FT /note= "wild type residue replaced with Ala"

XX WO200054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX PA
 XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX DR WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX Disclosure; Page 48-49; 73pp; English.
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA;
 SQ Query Match 88.3%; Score 316; DB 21; Length 70;
 Best Local Similarity 90.0%; Pred. No. 1.8e-33;
 Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIEKIPKYLFOFHNLSNL 60
 Db 1 TLVWGEFQVDSARGGCGTSAALAAALNASSKEALQIIEKIPKYLFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 Db 61 DRIFDKTPEP 70
 XX RESULT 13
 AAB18680
 ID AAB18680 standard; peptide; 70 AA.
 XX AC AAB18680;
 XX 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 FH Misc-difference 42
 FT /note= "wild type residue replaced with Ala"
 FT Misc-difference 43

OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 59 /note= "wild type residue replaced with Ala"
FT Misc-difference 61 /note= "wild type residue replaced with Ala"
FT Misc-difference 62 /note= "wild type residue replaced with Ala"
FT Misc-difference 62 /note= "wild type residue replaced with Ala"

XX WO200054573-A1.
FN
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYN-) UNIV NORTH CAROLINA STATE.
PA
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
FI
XX
XX WPI; 2000-618851/59.
DR
XX

Transgenic plants with increased resistance to geminivirus infection
comprise a nucleic acid construct containing a nucleic acid sequence
encoding a mutant AL1 protein with a mutation in the Rb binding region
-
_

Claim 53; Page 45; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.

SQ Sequence 70 AA;
Query Match 86.6%; Score 310; DB 21; Length 70;
Best Local Similarity 88.6%; Pred No. 1.1e-32;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 TLVNGEFOVDRSARGGQTSNDAAALAAASSAAALQIREKIPKYLQFHNLSNL 60
Db 1 TLVNGEFOVDRSARGGQTSNDAAALAAASSAAALQIREKIPKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 AAIFDKTPEP 70

Search completed: December 23, 2003, 08:56:29
Job time : 33.6667 secs

Db 110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRSL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 2

US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match 60.9%; Score 218; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. NO. 4.le-21;
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;
QY 1 TLWGFQVDGRSARGGQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 60
Db 110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRSL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 3

US-08-838-151A-6
; Sequence 6, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul

; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6

Query Match 60.9%; Score 218; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. NO. 4.le-21;
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;
QY 1 TLWGFQVDGRSARGGQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 60
Db 110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRSL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 4

US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```
; MOLECULE TYPE: protein
US-08-838-151A-44

Query Match      60.6%; Score 217; DB 3; Length 353;
Best Local Similarity 58.6%; Pred.No.5.4e-21;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY   1 TLVWGSEFVDGSRAGCGCOTSDNAAAAALAAASAAAALOIIREKIPEKYLFOFHNLNSNL 60
    :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db   110 TIEMGFQFDGSRAGCGQSANDSYAKALNADSIIESALTILKEEQKDVLQHNIIRSNL 169

QY   61 DRIFDKTPPE 70
    :|||||
Db   170 ERIFVKVPPE 179

RESULT 6
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-46

Query Match      60.6%; Score 217; DB 3; Length 353;
Best Local Similarity 58.6%; Pred.No.5.4e-21;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY   1 TLVWGSEFVDGSRAGCGCOTSDNAAAAALAAASAAAALOIIREKIPEKYLFOFHNLNSNL 60
    :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db   110 TIEMGFQFDGSRAGCGQSANDSYAKALNADSIIESALTILKEEQKDVLQHNIIRSNL 169

QY   61 DRIFDKTPPE 70
    :|||||
Db   170 ERIFVKVPPE 179
```

```
RESULT 7
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-49
; Query Match 60.6%; Score 217; DB 3; Length 353;
; Best Local Similarity 58.6%; Pred. No. 5.4e-21;
; Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
;
; QY 1 TLVWGEFQVGRSARGGCGTNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
; Db 110 TIEWGFQVGRSARGGCGQSANDSYAKALNADSIETSLTILKEQPKDYVLQHHNIRSNL 169
;
; QY 61 DRIFDKTPEP 70
; Db 170 ERIFVKVPEP 179
;
; RESULT 8
US-08-838-151A-52
; Sequence 52, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
```

```
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-52
; Query Match 60.6%; Score 217; DB 3; Length 353;
; Best Local Similarity 58.6%; Pred. No. 5.4e-21;
; Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
;
; QY 1 TLVWGEFQVGRSARGGCGTNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
; Db 110 TIEWGFQVGRSARGGCGQSANDSYAKALNADSIETSLTILKEQPKDYVLQHHNIRSNL 169
;
; QY 61 DRIFDKTPEP 70
; Db 170 ERIFVKVPEP 179
;
; RESULT 9
US-08-838-151A-55
; Sequence 55, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
```

RESULT 12

```

US-08-809-103B-6
; Sequence 6, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-6

Query Match          59.2%;   Score 212;   DB 3;   Length 359;
Best Local Similarity 56.5%;   Pred. No. 2.6e-20;
Matches 39;   Conservative 10;   Mismatches 20;   Indels 0;   Gaps 0;

Qy      2  LWGEGFQDGRSARGCGTSDNDAAAALAAASAAAALQIIRKIEKYLQFHNNLSNLD 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      111  LEWGTFTQDGRSARGGQQTANDAYAKAINAGSKSQALDVIRELAPRDYVYLHFHNNLSNLD 170
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      62  RIFDKTPRP 70
      :|||:|||||
Db      171  KVFQVPPAP 179

RESULT 13
US-08-809-103B-8
; Sequence 8, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia

```

```
/
/
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mueller, Lisa V
/ REGISTRATION NUMBER: 38,978
/ REFERENCE/DOCKET NUMBER: SVS3801P0260
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-616-5400
/ TELEFAX: 312-616-5460
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 357 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-838-151A-20

Query Match      53.1%; Score 190; DB 3; Length 357;
Best Local Similarity 60.7%; Pred. No. 2.4e-17;
Matches 37; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY      4 WGEFQV DGRSARGG CQTSDNDA AALAA SAAALQ IIREK IPEK YLFQ FHNLSNLDRI 63
Db      111 FGVSIQ DGRSARGG QQSANDAYAEALNSGSISEALN ILKEKAPKDYILQ FHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

RESULT 15
US-08-838-151A-24
/ Sequence 24, Application US/08838151A
/ Patent No. 6291743
/ GENERAL INFORMATION:
/ APPLICANT: Stout, John T
/ APPLICANT: Luu, Hang T
/ APPLICANT: Maxwell, Douglas
/ APPLICANT: Ahlquist, Paul
/ APPLICANT: Hanson, Steve
/ TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
/ TITLE OF INVENTION: Genes
/ NUMBER OF SEQUENCES: 63
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dressler, Rockey, Milnamow & Katz
/ STREET: Two Prudential Plaza, Suite 4700
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: U.S.A.
/ ZIP: 60601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/838,151A
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mueller, Lisa V
/ REGISTRATION NUMBER: 38,978
/ REFERENCE/DOCKET NUMBER: SVS3801P0260
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-616-5400
/ TELEFAX: 312-616-5460
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 357 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-838-151A-24
```

```
Query Match      53.1%; Score 190; DB 3; Length 357;
Best Local Similarity 60.7%; Pred. No. 2.4e-17;
Matches 37; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY      4 WGEFQV DGRSARGG CQTSDNDA AALAA SAAALQ IIREK IPEK YLFQ FHNLSNLDRI 63
Db      111 FGVSIQ DGRSARGG QQSANDAYAEALNSGSISEALN ILKEKAPKDYILQ FHNLSNLDRI 170

QY      64 F 64
Db      171 F 171
```

Search completed: December 23, 2003, 08:59:33
Job time : 12.6667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds
(without alignments)
172.015 Million cell updates/sec

US-09-289-346B-3

Title:

Perfect score: 358

Sequence:

1 TLVWGFQVDRSARGGCQT.....FQPHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	358	100.0	70	10	US-09-289-346A-3
2	347	96.9	70	10	US-09-289-346A-15
3	343	95.8	70	10	US-09-289-346A-14
4	332	92.7	70	10	US-09-289-346A-1
5	332	92.7	356	10	US-09-289-346A-11
6	324	90.5	70	10	US-09-289-346A-9
7	321	89.7	70	10	US-09-289-346A-12
8	320	89.4	70	10	US-09-289-346A-16
9	318	88.8	70	10	US-09-289-346A-8
10	317	88.5	70	10	US-09-289-346A-2
11	317	88.5	70	10	US-09-289-346A-10
12	316	88.3	70	10	US-09-289-346A-13
13	314	87.7	70	10	US-09-289-346A-4
14	311	86.9	70	10	US-09-289-346A-5
15	310	86.6	70	10	US-09-289-346A-7

16	308	86.0	70	10	US-09-289-346A-6
17	70.5	19.7	452	12	US-10-094-749-2809
18	66	18.4	1998	15	US-10-184-644-53
19	66	18.4	1998	15	US-10-184-634-53
20	66	18.4	3819	12	US-10-140-472-405
21	66	18.4	3819	12	US-10-141-761-405
22	66	18.4	3819	12	US-10-142-885-405
23	66	18.4	3819	12	US-10-158-790-405
24	66	18.4	3819	12	US-10-137-871-405
25	66	18.4	3819	12	US-10-140-805-405
26	66	18.4	3819	12	US-10-140-864-405
27	66	18.4	3819	12	US-10-140-923-405
28	66	18.4	3819	12	US-10-141-756-405
29	66	18.4	3819	12	US-10-141-759-405
30	66	18.4	3819	12	US-10-123-155-405
31	66	18.4	3819	16	US-10-146-731-405
32	65	18.2	3462	15	US-10-184-644-413
33	65	18.2	3462	15	US-10-184-634-413
34	64	17.9	972	15	US-10-184-644-443
35	64	17.9	972	15	US-10-184-634-443
36	64	17.9	1969	15	US-10-184-644-193
37	64	17.9	1969	15	US-10-184-634-193
38	64	17.9	3582	15	US-10-184-644-465
39	64	17.9	3582	15	US-10-184-634-465
40	63	17.6	21	10	US-09-984-056-17
41	63	17.6	21	10	US-09-984-057-17
42	63	17.6	21	12	US-10-185-232-17
43	63	17.6	21	12	US-10-189-437-17
44	63	17.6	886	15	US-10-156-761-9112
45	63	17.6	914	10	US-09-975-143-47

ALIGNMENTS

RESULT 1

US-09-289-346A-3
; Sequence 3, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (27)..(36)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (BALNASSKEE->AALAASSAAA)
US-09-289-346A-3

Query Match 100.0%; Score 358; DB 10; Length 70;

Best Local Similarity 100.0%; Pred. No. 8.9e-10; Indels 0; Gaps 0;
Matches 70; Conservative 0; Mismatches 0;

Qy 1 TLVWGFQVDRSARGGCQTSDAAAAAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60

Db 1 TLVWGFQVDRSARGGCQTSDAAAAAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60

Qy 61 DRIFDKTPEP 70

```
Db 61 DRIFDKTPEP 70
|||||
RESULT 2
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15
Query Match 96.9%; Score 347; DB 10; Length 70;
Best Local Similarity 97.1%; Pred. No. 2.4e-37;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDCRSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVDCRSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
|||||
Db 61 DRIFDKTPEP 70
|||||
RESULT 3
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14
Query Match 95.8%; Score 343; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 7.8e-37;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDCRSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVDCRSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
|||||
Db 61 DRIFDKTPEP 70
|||||
RESULT 4
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11
Query Match 92.7%; Score 332; DB 10; Length 356;
Best Local Similarity 92.9%; Pred. No. 1.6e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDCRSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Db 110 TLVWGEFQVDCRSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 169
QY 61 DRIFDKTPEP 70
|||||
Db 61 DRIFDKTPEP 70
|||||
RESULT 5
US-9-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11
Query Match 92.7%; Score 332; DB 10; Length 356;
Best Local Similarity 92.9%; Pred. No. 1.6e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDCRSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Db 110 TLVWGEFQVDCRSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 169
```



```

QY      61 DRIFDKTPEP 70
Db      170 DRIFDKTPEP 179

RESULT 6
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRP
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match      90.5%; Score 324; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 2.2e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 TLVWGFQVDGRSARGCGQTSNDAAAALAAASSAAAALQIIREKIPEKYLQFHNLSNL 60
Db      1 TLVWGFQVDGRSARGCGQTSNDAAAALAAASSAAAALQIIREKIPEKYLQFHNLSNL 60

RESULT 7
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRP
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12

Query Match      89.7%; Score 321; DB 10; Length 70;
Best Local Similarity 90.0%; Pred. No. 5.5e-34;

QY      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

RESULT 8
US-09-289-346A-16
; Sequence 16, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 70
; TYPE: PRP
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-16

Query Match      89.4%; Score 320; DB 10; Length 70;
Best Local Similarity 90.0%; Pred. No. 7.4e-34;
Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 TLVWGFQVDGRSARGCGQTSNDAAAALAAASSAAAALQIIREKIPEKYLQFHNLSNL 60
Db      1 TLVWGFQVDGRSARGCGQTSNDAAAALAAASSAAAALQIIREKIPEKYLQFHNLSNL 60

RESULT 9
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRP
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine

```

INVENTOR: GREGORY, WILLIAM

TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS

```
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; NAME/KEY: VARIANT
; LOCATION: (42)..(44)
; OTHER INFORMATION: Description of Artificial sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAA154).
US-09-289-346A-4

Query Match      87.7%; Score 314; DB 10; Length 70;
Best Local Similarity 88.6%; Pred. No. 4.4e-33;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSGCGCQTSNDAAAALAAASSAAAAAQIIREKIPKYLQFHNLSNL 60
Db 1 TLVWGEFQVDRSGCGCQTSNDAAAALAAASSAAAAAQIIREKIPKYLQFHNLSNL 60

Qy 61 DRIPDKTPEP 70
Db 61 DRIPDKTPEP 70

RESULT 14
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (SKY159->AAA159).
US-09-289-346A-5

Query Match      86.9%; Score 311; DB 10; Length 70;
Best Local Similarity 88.6%; Pred. No. 1.1e-32;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSGCGCQTSNDAAAALAAASSAAAAAQIIREKIPKYLQFHNLSNL 60
Db 1 TLVWGEFQVDRSGCGCQTSNDAAAALAAASSAAAAAQIIREKIPKYLQFHNLSNL 60

Qy 61 DRIPDKTPEP 70
Db 61 DRIPDKTPEP 70
```

```
RESULT 15
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDR172->ALAA172).
US-09-289-346A-7

Query Match      86.6%; Score 310; DB 10; Length 70;
Best Local Similarity 88.6%; Pred. No. 1.1e-32;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSGCGCQTSNDAAAALAAASSAAAAAQIIREKIPKYLQFHNLSNL 60
Db 1 TLVWGEFQVDRSGCGCQTSNDAAAALAAASSAAAAAQIIREKIPKYLQFHNLSNL 60

Qy 61 DRIPDKTPEP 70
Db 61 DRIPDKTPEP 70

Search completed: December 23, 2003, 09:43:29
Job time : 77 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:56:38 ; Search time 163.778 Seconds
(without alignments)
388.907 Million cell updates/sec

Title: US-09-289-346B-3

Perfect score: 358

Sequence: 1 TLVWGEFQVDSRGSCQT.....FQPHNLNLDRIPTKPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/paa/PCTUS COMB.pcp.*
2: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
3: /cgn2_6/ptodata/1/paa/US07 COMB.pcp.*
4: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
5: /cgn2_6/ptodata/1/paa/US081 COMB.pcp.*
6: /cgn2_6/ptodata/1/paa/US082 COMB.pcp.*
7: /cgn2_6/ptodata/1/paa/US083 COMB.pcp.*
8: /cgn2_6/ptodata/1/paa/US084 COMB.pcp.*
9: /cgn2_6/ptodata/1/paa/US085 COMB.pcp.*
10: /cgn2_6/ptodata/1/paa/US086 COMB.pcp.*
11: /cgn2_6/ptodata/1/paa/US087 COMB.pcp.*
12: /cgn2_6/ptodata/1/paa/US088 COMB.pcp.*
13: /cgn2_6/ptodata/1/paa/US089 COMB.pcp.*
14: /cgn2_6/ptodata/1/paa/US090 COMB.pcp.*
15: /cgn2_6/ptodata/1/paa/US091 COMB.pcp.*
16: /cgn2_6/ptodata/1/paa/US092 COMB.pcp.*
17: /cgn2_6/ptodata/1/paa/US093 COMB.pcp.*
18: /cgn2_6/ptodata/1/paa/US094 COMB.pcp.*
19: /cgn2_6/ptodata/1/paa/US095 COMB.pcp.*
20: /cgn2_6/ptodata/1/paa/US096 COMB.pcp.*
21: /cgn2_6/ptodata/1/paa/US097A COMB.pcp.*
22: /cgn2_6/ptodata/1/paa/US097B COMB.pcp.*
23: /cgn2_6/ptodata/1/paa/US098 COMB.pcp.*
24: /cgn2_6/ptodata/1/paa/US099A COMB.pcp.*
25: /cgn2_6/ptodata/1/paa/US099B COMB.pcp.*
26: /cgn2_6/ptodata/1/paa/US100 COMB.pcp.*
27: /cgn2_6/ptodata/1/paa/US101 COMB.pcp.*
28: /cgn2_6/ptodata/1/paa/US102 COMB.pcp.*
29: /cgn2_6/ptodata/1/paa/US103 COMB.pcp.*
30: /cgn2_6/ptodata/1/paa/US104 COMB.pcp.*
31: /cgn2_6/ptodata/1/paa/US106 COMB.pcp.*
32: /cgn2_6/ptodata/1/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	358	100.0	70	16	US-09-289-346A-3

Sequence 3, Appli

2	358	100.0	70	31	US-10-633-850-4	Sequence 4, Appli
3	358	100.0	352	31	US-10-633-850-78	Sequence 78, Appli
4	347	96.9	70	16	US-09-289-346A-15	Sequence 15, Appli
5	347	96.9	70	31	US-10-633-850-15	Sequence 15, Appli
6	347	96.9	352	31	US-10-633-850-64	Sequence 64, Appli
7	343	95.8	70	16	US-09-289-346A-14	Sequence 14, Appli
8	343	95.8	70	31	US-10-633-850-14	Sequence 14, Appli
9	343	95.8	352	31	US-10-633-850-62	Sequence 62, Appli
10	342	95.5	70	31	US-10-633-850-20	Sequence 20, Appli
11	342	95.5	352	31	US-10-633-850-86	Sequence 86, Appli
12	337	94.1	70	31	US-10-633-850-17	Sequence 17, Appli
13	337	94.1	70	31	US-10-633-850-18	Sequence 18, Appli
14	337	94.1	70	31	US-10-633-850-19	Sequence 19, Appli
15	337	94.1	352	31	US-10-633-850-80	Sequence 80, Appli
16	337	94.1	352	31	US-10-633-850-82	Sequence 82, Appli
17	337	94.1	352	31	US-10-633-850-84	Sequence 84, Appli
18	332	92.7	70	16	US-09-289-346A-1	Sequence 1, Appli
19	332	92.7	70	31	US-10-633-850-2	Sequence 2, Appli
20	332	92.7	352	31	US-10-633-850-1	Sequence 1, Appli
21	332	92.7	356	16	US-09-289-346A-11	Sequence 11, Appli
22	329	91.9	70	31	US-10-633-850-23	Sequence 23, Appli
23	329	91.9	352	31	US-10-633-850-92	Sequence 92, Appli
24	329	91.9	352	31	US-10-633-850-94	Sequence 94, Appli
25	327	91.3	70	31	US-10-633-850-22	Sequence 22, Appli
26	327	91.3	352	31	US-10-633-850-90	Sequence 90, Appli
27	326	91.1	70	31	US-10-633-850-21	Sequence 21, Appli
28	326	91.1	352	31	US-10-633-850-88	Sequence 88, Appli
29	324	90.5	70	16	US-09-289-346A-9	Sequence 9, Appli
30	324	90.5	70	31	US-10-633-850-10	Sequence 10, Appli
31	324	90.5	70	31	US-10-633-850-24	Sequence 24, Appli
32	324	90.5	352	31	US-10-633-850-96	Sequence 96, Appli
33	322	89.9	70	31	US-10-633-850-25	Sequence 25, Appli
34	322	89.9	352	31	US-10-633-850-98	Sequence 98, Appli
35	321	89.7	70	16	US-09-289-346A-12	Sequence 12, Appli
36	321	89.7	70	31	US-10-633-850-12	Sequence 12, Appli
37	321	89.7	352	31	US-10-633-850-58	Sequence 58, Appli
38	320	89.4	70	16	US-09-289-346A-16	Sequence 16, Appli
39	320	89.4	70	31	US-10-633-850-16	Sequence 16, Appli
40	320	89.4	352	31	US-10-633-850-74	Sequence 74, Appli
41	318	88.8	70	16	US-09-289-346A-8	Sequence 8, Appli
42	318	88.8	70	31	US-10-633-850-9	Sequence 9, Appli
43	318	88.8	352	31	US-10-633-850-52	Sequence 52, Appli
44	317	88.5	70	16	US-09-289-346A-2	Sequence 2, Appli
45	317	88.5	70	16	US-09-289-346A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-289-346A-3
; GENERAL INFORMATION:
; SEQUENCE 3, Application US/09289346A
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (27)-(36)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of

```
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (EALNASSKEE->AALAASSAAA)
US-09-289-346A-3

Query Match          100.0%; Score 358; DB 16; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e-38; Indels 0; Gaps 0;
Matches 70; Conservative 0; Mismatches 0;

QY 1 TLVWGEFQVDRSARGCQTSNDAAALAAASSAAAALQIIREKIPEKYLQFPHNLSNL 60
   |||||||
Db 1 TLVWGEFQVDRSARGCQTSNDAAALAAASSAAAALQIIREKIPEKYLQFPHNLSNL 60
   |||||||

QY 61 DRIFDKTPEP 70
   |||||||
Db 61 DRIFDKTPEP 70

RESULT 2
US-10-633-850-4
; Sequence 4, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.458IP
; CURRENT APPLICATION NUMBER: US/10/633,850
; PRIOR FILING DATE: 2003-08-04
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: MICS_FEATURE
; LOCATION: (27)..(36)
; OTHER INFORMATION: E-N140 + KEE146 (Ala4+5) mutation
US-10-633-850-4

Query Match          100.0%; Score 358; DB 31; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e-38; Indels 0; Gaps 0;
Matches 70; Conservative 0; Mismatches 0;

QY 1 TLVWGEFQVDRSARGCQTSNDAAALAAASSAAAALQIIREKIPEKYLQFPHNLSNL 60
   |||||||
Db 1 TLVWGEFQVDRSARGCQTSNDAAALAAASSAAAALQIIREKIPEKYLQFPHNLSNL 60
   |||||||

QY 61 DRIFDKTPEP 70
   |||||||
Db 61 DRIFDKTPEP 70

RESULT 3
US-10-633-850-78
; Sequence 78, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.458IP
; CURRENT APPLICATION NUMBER: US/10/633,850
; PRIOR FILING DATE: 2003-08-04
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: MICS_FEATURE
; LOCATION: (27)..(36)
; OTHER INFORMATION: E-N140 + KEE146 (Ala4+5) mutation
US-10-633-850-78

Query Match          96.9%; Score 347; DB 16; Length 70;
Best Local Similarity 97.1%; Pred. No. 4.2e-37; Indels 0; Gaps 0;
Matches 68; Conservative 0; Mismatches 2;

QY 1 TLVWGEFQVDRSARGCQTSNDAAALAAASSAAAALQIIREKIPEKYLQFPHNLSNL 60
   |||||||
Db 1 TLVWGEFQVDRSARGCQTSNDAAALAAASSAAAALQIIREKIPEKYLQFPHNLSNL 60
   |||||||

QY 61 DRIFDKTPEP 70
   |||||||
Db 61 DRIFDKTPEP 70

RESULT 4
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match          96.9%; Score 347; DB 16; Length 70;
Best Local Similarity 97.1%; Pred. No. 4.2e-37; Indels 0; Gaps 0;
Matches 68; Conservative 0; Mismatches 2;

QY 1 TLVWGEFQVDRSARGCQTSNDAAALAAASSAAAALQIIREKIPEKYLQFPHNLSNL 60
   |||||||
Db 1 TLVWGEFQVDRSARGCQTSNDAAALAAASSAAAALQIIREKIPEKYLQFPHNLSNL 60
   |||||||

QY 61 DRIFDKTPEP 70
   |||||||
Db 61 DRIFDKTPEP 70

RESULT 5
US-10-633-850-15
; Sequence 15, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.458IP
; CURRENT APPLICATION NUMBER: US/10/633,850
; PRIOR FILING DATE: 2003-08-04
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-10-633-850-15

Query Match          100.0%; Score 358; DB 16; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e-38; Indels 0; Gaps 0;
Matches 70; Conservative 0; Mismatches 0;

QY 1 TLVWGEFQVDRSARGCQTSNDAAALAAASSAAAALQIIREKIPEKYLQFPHNLSNL 60
   |||||||
Db 1 TLVWGEFQVDRSARGCQTSNDAAALAAASSAAAALQIIREKIPEKYLQFPHNLSNL 60
   |||||||

QY 61 DRIFDKTPEP 70
   |||||||
Db 61 DRIFDKTPEP 70
```

```
; LENGTH: 70
; TYPE: PRF
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (34)..(36)
; OTHER INFORMATION: KEE146 (Ala5) mutation
US-10-633-850-15

Query Match      96.9%; Score 347; DB 31; Length 70;
Best Local Similarity 97.1%; Pred. No. 4.2e-37;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 6
US-10-633-850-64
; Sequence 64, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 352
; TYPE: PRF
; ORGANISM: Tomato golden mosaic virus
US-10-633-850-64

Query Match      96.9%; Score 347; DB 31; Length 352;
Best Local Similarity 97.1%; Pred. No. 3.4e-36;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Db 111 TLVWGFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 170
Qy 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180

RESULT 7
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRF
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match      95.8%; Score 343; DB 16; Length 70;
Best Local Similarity 95.7%; Pred. No. 1.4e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 8
US-10-633-850-14
; Sequence 14, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRF
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (27)..(30)
; OTHER INFORMATION: E--N140 (Ala4) mutation
US-10-633-850-14

Query Match      95.8%; Score 343; DB 31; Length 70;
Best Local Similarity 95.7%; Pred. No. 1.4e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 9
US-10-633-850-62
; Sequence 62, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
```

```
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-10-633-850-62

Query Match          95.8%; Score 343; DB 31; Length 352;
Best Local Similarity 95.7%; Pred. No. 1.1e-35;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGCOTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60
Db 111 TLVWGEFQVDSARGCGCOTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 170
QY 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180

RESULT 10
US-10-633-850-20
; Sequence 20, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.458IP
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (35)..(36)
; OTHER INFORMATION: EE146 mutation
US-10-633-850-20

Query Match          95.5%; Score 342; DB 31; Length 70;
Best Local Similarity 95.7%; Pred. No. 1.9e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGCOTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGEFQVDSARGCGCOTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 11
US-10-633-850-86
; Sequence 86, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.458IP
; CURRENT APPLICATION NUMBER: US/10/633,850
```

```
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-10-633-850-86

Query Match          95.5%; Score 342; DB 31; Length 352;
Best Local Similarity 95.7%; Pred. No. 1.5e-35;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGCOTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60
Db 111 TLVWGEFQVDSARGCGCOTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 170
QY 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180

RESULT 12
US-10-633-850-17
; Sequence 17, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.458IP
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (34)..(34)
; OTHER INFORMATION: K144 mutation
US-10-633-850-17

Query Match          94.1%; Score 337; DB 31; Length 70;
Best Local Similarity 94.3%; Pred. No. 8.6e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGCOTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGEFQVDSARGCGCOTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 13
US-10-633-850-18
; Sequence 18, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
```

; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.458IP
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (35)..(35)
; OTHER INFORMATION: E145 mutation
US-10-633-850-18

Query Match 94.1%; Score 337; DB 31; Length 70;
Best Local Similarity 94.3%; Pred. No. 8.6e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TLVWGFQVDRSARGCGCQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGFQVDRSARGCGCQTSNDAAAALNASSKAAALQIIREKIPEKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 14
US-10-633-850-19
; Sequence 19, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.458IP
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (36)..(36)
; OTHER INFORMATION: E146 mutation
US-10-633-850-19

Query Match 94.1%; Score 337; DB 31; Length 70;
Best Local Similarity 94.3%; Pred. No. 8.6e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TLVWGFQVDRSARGCGCQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGFQVDRSARGCGCQTSNDAAAALNASSKAAALQIIREKIPEKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 15
US-10-633-850-80
; Sequence 80, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.458IP
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-10-633-850-80

Query Match 94.1%; Score 337; DB 31; Length 352;
Best Local Similarity 94.3%; Pred. No. 7e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TLVWGFQVDRSARGCGCQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Db 111 TLVWGFQVDRSARGCGCQTSNDAAAALNASSKAAALQIIREKIPEKYLQFHNLSNL 170
Qy 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180

Search completed: December 23, 2003, 09:30:02
Job time : 163.778 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds
(without alignments)
673.181 Million cell updates/sec

Title: US-09-289-346B-3
Perfect score: 358
Sequence: 1 TLVWGEFQVDSARGGCQT.....FQPHNLNSLDRIFDKTPEP 70

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: Piri:.*
2: Piri:.*
3: Piri:.*
4: Piri:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	332	92.7	352	1 QOCVLI	AlI protein - toma
2	243	67.9	361	1 QOCVPT	AlI protein - toma
3	230	64.2	358	2 S07594	hypothetical prote
4	222	62.0	362	1 JQ1887	AlI protein - toma
5	217	60.6	355	1 QOCVM1	AVI protein - abut
6	216	60.3	349	2 JQ2300	replicase - pepp
7	216	60.3	349	2 S31875	AlI protein - pepp
8	216	60.3	359	2 S39211	gene C1 protein -
9	214	59.8	358	1 JQ1870	AlI protein - toma
10	213	59.5	351	2 JQ2327	AlI protein - Indi
11	212	59.2	359	2 S22593	hypothetical prote
12	208	58.1	365	2 S28360	AlI protein - beet
13	207	57.8	360	2 S59885	replication-associ
14	203	56.7	359	2 S39235	gene C1 protein -
15	190	53.1	357	1 QOCVC1	AlI protein - toma
16	120	33.5	131	2 S45059	AC1 protein (clone
17	115	32.1	347	1 QOCVS1	AlI protein - aqua
18	69	19.3	577	2 S30237	transcription init
19	66	18.4	508	2 S59870	fork head domain p
20	66	18.4	840	2 T36375	probable large ATP
21	65	18.2	254	2 F97486	DNA repair protein
22	65	18.2	254	2 F97486	reco-like protein
23	65	18.2	671	2 A35912	homeotic protein o
24	63	17.6	392	2 T44362	acetyl-CoA C-acety
25	62.5	17.5	700	2 T05841	aplicosome-associ
26	62.5	17.5	1077	2 A44067	serine-rich protei
27	62	17.3	409	2 T16781	hypothetical prote
28	61.5	17.2	317	2 D89961	conserved hypothet
29	61.5	17.2	327	2 P83408	hypothetical prote

30	61.5	17.2	705	2 T31157	hypothetical prote
31	61.5	17.2	1541	2 T02831	AAA protein I4171.
32	61	17.0	339	2 T26328	hypothetical prote
33	61	17.0	371	2 B69502	alcohol dehydrogen
34	61	17.0	1265	2 T47626	structural mainten
35	61	17.0	1510	2 T33100	hypothetical prote
36	60.5	16.9	509	2 T02942	O-succinylhomoseri
37	60.5	16.9	829	2 A34692	ecdysone-induced p
38	60.5	16.9	883	2 S04722	puff 74E protein -
39	60	16.8	314	2 JCS273	paired type homsob
40	59.5	16.6	201	2 A81380	probable flagellar
41	59.5	16.6	244	2 B86197	hypothetical prote
42	59.5	16.6	470	2 T46814	gamma-aminobutyrat
43	59.5	16.6	470	2 B95419	diaminobutyrate-py
44	59.5	16.6	481	2 A70091	probable phosphoes
45	59.5	16.6	509	2 T02940	O-succinylhomoseri

ALIGNMENTS

RESULT 1

QOCVLI
AlI protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994
C:Accession: A04170
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
A:Residues: 1-352 <HAM>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AlI protein

Query Match 92.7%; Score 332; DB 1; Length 352;
Best Local Similarity 92.9%; Pred. No. 4.8e-31;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 TLVWGEFQVDSARGGCQTSNDAAAALAAASAAAALQIIRKIPKYLQFPHNLNSL 60
Db 111 TLVWGEFQVDSARGGCQTSNDAAAALAAASAAAALQIIRKIPKYLQFPHNLNSL 170
Qy 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180

RESULT 2

QOCVPT
AlI protein - potato yellow mosaic virus (isolate Venezuela)
C:Species: potato yellow mosaic virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C:Accession: JU0364
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel
A:Reference number: JU0362; MUID:91311403; PMID:1856690
A:Accession: JU0364
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-361 <COU>
A:Cross-references: GB:D00940; NID:G222458; PIDN:BAA00782.1; PID:G222459
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AlI protein

```
Query Match      67.9%; Score 243; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 1.2e-20;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 110 TLEWGFQIDGRSARGGQQTVDNAAALNKGKAAKIIKEKLPKFLFOYHNLSNL 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 DRIFDKTPEP 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 DRIFWKAPE 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
S07594
hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)
C:Species: cassava latent virus
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C:Accession: S07594
R:Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
Nucleic Acids Res. 18, 197-198, 1990
A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A:Reference number: S07590; MUID:90174950; PMID:2308831
A:Accession: S07594
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <MOR>
A:Cross-references: EMBL:X17095; NID:G59371; PIDN:CAA34953.1; PID:G59376
C:Genetics:
A:Map position: segment DNA1
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match      64.2%; Score 230; DB 2; Length 358;
Best Local Similarity 60.0%; Pred. No. 4e-19;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 109 TVEWGFQIDGRSARGGQTSNDAAALNKGKSEALNIRELVKPKVLFQFHNLSNL 168
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 DRIFDKTPEP 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 169 DRIFQEPAP 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
JQ1887
AL1 protein - tomato yellow leaf curl virus (strain Australia)
N:Alternate names: C1 protein
C:Species: tomato yellow leaf curl virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
C:Accession: JQ1887
R:Dry, I.B.; Rigden, J.E.; Krake, L.R.; Mullineaux, P.M.; Rezaian, M.A.
J. Gen. Virol. 74, 147-151, 1993
A:Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.
A:Reference number: JQ1885; MUID:93139778; PMID:8423446
A:Accession: JQ1887
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <DRY>
A:Cross-references: GB:S53251
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match      62.0%; Score 222; DB 1; Length 362;
Best Local Similarity 52.9%; Pred. No. 3.5e-18;
Matches 45; Conservative 9; Mismatches 15; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 110 TLEWGFQIDGRSARGGQTSNDAAALNKGKSEALNIRELVKPKVLFQFHNLSNL 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 DRI-----FDKTPPE 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Db 170 DRIFTPPLEVYVSPFLSSSFDVRPE 194
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
QOCQVM1
AV1 protein - abutilon mosaic virus (isolate West India)
C:Species: abutilon mosaic virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Apr-1994
C:Accession: A36214
R:Frischmuth, T.; Zimmatt, G.; Jeske, H.
Virology 178, 461-468, 1990
A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as we
A:Reference number: A36214; MUID:91020984; PMID:2219703
A:Accession: A36214
A:Molecule type: DNA
A:Residues: 1-355 <FRI>
A:Cross-references: EMBL:X15983
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match      60.6%; Score 217; DB 1; Length 355;
Best Local Similarity 58.6%; Pred. No. 1.3e-17;
Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 110 TAEWGEFQIDGRSARGGQQTANDSYAKALNAGDVQSALNILEEQPKOYVQLQNHIRSNL 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 DRIFDKTPEP 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 ERIFAKAPEP 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
JQ2300
replicase - pepper huasteco virus (component A)
N:Alternate names: ORF AL1 protein
C:Species: pepper huasteco virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Sep-1999
C:Accession: JQ2300
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estrella, L.; Rivera-Bustamante, R.
J. Gen. Virol. 74, 2225-2231, 1993
A:Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with b1f
A:Reference number: JQ2299; MUID:94015007; PMID:8409944
A:Accession: JQ2300
A:Molecule type: DNA
A:Residues: 1-349 <TOR>
A:Cross-references: GB:X70418; NID:961023; PIDN:CAA49856.1; PID:G61025
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match      60.3%; Score 216; DB 2; Length 349;
Best Local Similarity 58.6%; Pred. No. 1.7e-17;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 110 TVEWGEFQIDGRSARGGQTSNDTYAKALNSASAEALQIIEEQPKHFLFOFHNIVSNA 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 DRIFDKTPEP 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 NRIFQTPPEP 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
S31875
AL1 protein - pepper rizado amarillo virus
C:Species: pepper rizado amarillo virus
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 20-Sep-1999
C:Accession: S31875
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-E
submitted to the EMBL Data Library, February 1993
A:Description: Complete nucleotide sequence of pepper huasteco virus: analysis and comp
```

A;Reference number: S31872
A;Accession: S31875
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <TOR>
A;Cross-references: EMBL:X70418; NID:g61023; PIDN:CAA49856.1; PID:g61025
A;Note: the source is designated as pepper huasteco virus
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 60.3%; Score 216; DB 2; Length 349;
Best Local Similarity 58.6%; Pred. No. 1.7e-17;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
DB 110 TVEFGFQIDGRSARGGQSANDYAKALNSASAEALQIIREKIPKYLQFHNLSNA 169

QY 61 DRIFDKTPEP 70
DB 170 NRIFQTPPEP 179

RESULT 8
S39211
gene C1 protein - tomato yellow leaf curl virus
C;Species: tomato yellow leaf curl virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C;Accession: S39211
R;Noris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.
submitted to the EMBL Data Library, August 1993
A;Description: High similarity among the tomato yellow leaf curl virus isolates from the
A;Reference number: S39209
A;Accession: S39211
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <NOR>
A;Cross-references: EMBL:Z25751; NID:g433655; PIDN:CAA81026.1; PID:g433658
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 60.3%; Score 216; DB 2; Length 359;
Best Local Similarity 58.0%; Pred. No. 1.8e-17;
Matches 40; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 61
DB 111 LEWGTQIDGRSARGGQQTANDAYAKINAGSKSEALDKELAPRDYILHFNHNSNL 170

QY 62 RIFDKTPEP 70
DB 171 RVFQVPPAP 179

RESULT 9
JQ1870
AL1 protein - tomato mottle virus (isolate Florida)
C;Species: tomato mottle virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
C;Accession: JQ1870
R;Abouzeid, A.M.; Polston, J.E.; Hiebert, E.
J. Gen. Virol. 73, 3225-3229, 1992
A;Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated from
A;Reference number: JQ1869; MUID:93107858; PMID:1469361
A;Accession: JQ1870
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-358 <ABO>
A;Cross-references: GB:I14460
C;Genetics:
A;Map position: segment A
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.8%; Score 214; DB 1; Length 358;
Best Local Similarity 55.7%; Pred. No. 3e-17;

Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLWGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
DB 107 TIEWGDFQIDGRSARGGQSANDYAKALNAGSVQSALAVLRERQPKDFVLQHNIRSNL 166

QY 61 DRIFDKTPEP 70
DB 167 ERIFAKAPEP 176

RESULT 10
JQ2327
AL1 protein - Indian cassava mosaic virus
N;Alternate names: replication-associated protein
C;Species: Indian cassava mosaic virus
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 20-Sep-1999
C;Accession: JQ2327; S35883
R;Hong, Y.G.; Robinson, D.J.; Harrison, B.D.
J. Gen. Virol. 74, 2437-2443, 1993
A;Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-tr
A;Reference number: JQ2326; MUID:94065670; PMID:8245859
A;Accession: JQ2327
A;Molecule type: DNA
A;Residues: 1-351 <HON>
A;Cross-references: EMBL:Z24758; NID:g395351; PIDN:CAA80891.1; PID:g584046
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.5%; Score 213; DB 2; Length 351;
Best Local Similarity 61.2%; Pred. No. 3.8e-17;
Matches 41; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 4 WGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 63
DB 113 WGTQFIDGRSARGGQSANDYAKALNAGSKSEALDKELAPRDYILHFNHNSNL 172

QY 64 FDKTPEP 70
DB 173 FTKPPPP 179

RESULT 11
S22593
hypothetical protein C4 - tomato yellow leaf curl virus
C;Species: tomato yellow leaf curl virus
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999
C;Accession: S22593
R;Kheyr-Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, I
Nucleic Acids Res. 19, 6763-6769, 1991
A;Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopar
A;Reference number: S22588; MUID:92107660; PMID:1840676
A;Accession: S22593
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-359 <KHE>
A;Cross-references: EMBL:X61153; NID:g62211; PIDN:CAA43466.1; PID:g62217
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.2%; Score 212; DB 2; Length 359;
Best Local Similarity 56.5%; Pred. No. 5.2e-17;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 61
DB 111 LEWGTQIDGRSARGGQQTANDAYAKINAGSKSQALDKELAPRDYILHFNHNSNL 170

QY 62 RIFDKTPEP 70
DB 171 RVFQVPPAP 179

RESULT 12

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds
(without alignments)
569.747 Million cell updates/sec

Title: US-09-289-346B-3

Perfect score: 358

Sequence: 1 TLVWGEFQVDGRSARGGCQT.....FQFHNLNSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62

Scoring cards: 2000002
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Minimum DB seq	length: 0
Maximum DB seq	length: 2000000000

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%

MAXIMUM MATCH 100%
Listing first 45 summaries

Database : SwissProt 41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	§			ID	Description
				Length	DB			
1	332	92.7	352	1	VALL1	TGMV	P03567	tomato gold
2	243	67.9	361	1	VALL1	PMWV	P27258	potato yell
3	230	64.2	358	1	VALL1	CLVK	P14982	cassava lat
4	230	64.2	358	1	VALL1	CLVN	P14972	cassava lat
5	222	62.0	362	1	VALL1	TYLVC	P36279	tomato yell
6	217	60.6	355	1	VALL1	ABWV	P21947	abutilon mo
7	216	60.3	349	1	VALL1	PHUV	P06923	pepper huas
8	215	60.3	359	1	VALL1	TYLCU	P38609	tomato yell
9	215	60.1	353	1	VALL1	BGMV	P05175	bean golden
10	214	59.8	361	1	VALL1	TMOV	P05175	bean golden
11	212	59.2	359	1	VALL1	TYLMC	P06657	tomato mott
12	208	58.1	358	1	VALL1	BCTV	P27260	tomato yell
13	190	53.1	357	1	VALL1	TYLVC	P14991	beet curly
14	115	32.1	347	1	VALL1	SICV	P27259	tomato yell
15	70.5	19.7	466	1	SPBH	HUMAN	P23048	squash leaf
16	70.5	19.7	486	1	SPBH	MOUSE	Q81xz3	homo sapien
17	69	19.3	577	1	T2FA	DROME	Q8Bmj8	homo musculu
18	66	18.4	207	1	IL6	MARMO	Q05913	drosoophila
19	66	18.4	508	1	CROC	DROME	Q05736	marmota mon
20	65	18.2	671	1	HMOC	DROME	P32027	drosoophila
21	62.5	17.5	1077	1	HLSS	DROME	P22810	drosoophila
22	60.5	16.9	829	1	E74A	DROME	Q02308	drosoophila
23	60.5	16.9	883	1	E74B	DROME	P20105	drosoophila
24	60	16.8	314	1	PMXB	HUMAN	P11536	drosoophila
25	60	16.8	314	1	PMXB	MOUSE	Q99453	homo sapien
26	59.5	16.6	470	1	RHBA	RHIME	Q35690	mus musculu
27	59	16.5	379	1	CYB	ASTPE	Q923r2	r diaminobu
28	59	16.5	498	1	CALR	PIG	Q33818	asterina pe
29	59	16.5	513	1	HEMO	CHICK	P25117	sus scrofa
30	59	16.5	3591	1	FHAB	BORPE	P18080	gallus gall
31	58.5	16.3	297	1	MEL	DROME	P12255	bordetella
32	58.5	16.3	478	1	RDPI	SCHPO	OL6011	drosoophila
33	58.5	16.3	1264	1	MOLR	ECOLI	O13862	schizosacch
34	58.5	16.3	1264	1	MOLR	ECOLI	P33345	escherichia

	34	35	36	37	38	39	40	41	42	43	44	45
	58.5	58	58	58	57.5	57.5	57.5	57.5	57.5	57.5	57	57
	16.3	16.2	16.2	16.2	16.1	16.1	16.1	16.1	16.1	16.1	15.9	15.9
	1713	732	731	1081	1392	303	338	557	601	1556	387	401
	1	1	1	1	1	1	1	1	1	1	1	1
	LMA3_HUMAN	CYG4_HUMAN	U052_HSVB	TRIB_HUMAN	ALB3_NAI2E	ALB3_NAI2E	HXB3_HUMAN	SAB3_ANAPL	DR11_HUMAN	PROS_DROVI	HVE1_MOUSE	HVE1_MOUSE
	Q16787	Q3402	P28962	Q14669	P10593	P10593	P31277	Q4791	Q39856	Q62431	Q9641	P09065
	homo sapien	homo sapien	equine herp	homo sapien	zea mays (m	zea mays (m	homo sapien	anas platyr	homo sapien	mus musculus	mus musculus	mus musculus

ALIGNMENTS

RESULT 1

```

VAL1_TGMV
ID VAL1_TGMV STANDARD; PRRT; 352 AA.
AC P03567;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE All protein.
DS
GN AC1.
OS Tomato golden mosaic virus (TGMV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10831;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;
RT "Complete nucleotide sequence of the infectious cloned DNA components
RT of tomato golden mosaic virus: potential coding regions and regulatory
RT sequences."
RT ENBO J. 3:2197-2205(1984).
RL
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

CC	EMBL; K02029; --; NOT_ANNOTATED_CDS.
DR	FIR; A04170; QOCVII.
DR	InterPro; IPR001191; Gemini_AL1.
DR	Pfam; PF00799; Gemini_AL1; 1.
DR	PRINTS; PR00227; GEMCOATALL.
DR	ProDom; PD000736; Gemini_AL1; 1.
KW	ATP-binding.
FT	NP_BIND 223 230 ATP (POTENTIAL).
SQ	SEQUENCE 352 AA; 40332 MW; C3C3938E9644B4A4 CRC64;

Query Match 92.7%; Score 332; DB 1; Length 352;
Best Local Similarity 92.9%; Pred. No. 1.2e-31;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAAAAQIIREKIPEKYLFOFHNLSNL 60
|||||
Db 111 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAAAAQIIREKIPEKYLFOFHNLSNL 170
|||||

RESULT 2

RESULT 2	
VAL1_PYMV	
ID VAL1_PYMV	STANDARD;
AC P27258;	PRT; 361 AA.

```
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus.";
RL J. Gen. Virol. 72:1515-1520(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D00940; BAA00782.1; -.
DR F1R; J00364; Q0CVPT.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;

Query Match 67.9%; Score 243; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 3.8e-21;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGRGCGTSDNDAALAAASAAALQIIRKIPKYLQFQHNLSNL 60
DB 110 TLVWGLFQIDGRSARGGQGVNDAAALNSGKTEAAKIKELPEKLFQVHNLSNL 169
QY 61 DRIFDKTPE 69
DB 170 DRIFDKAPE 178

RESULT 3
VAL1_CLVK STANDARD; PRT; 358 AA.
AC P149E2;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

```
CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753BE92D69 CRC64;

Query Match 64.2%; Score 230; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 1.3e-19;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGRGCGTSDNDAALAAASAAALQIIRKIPKYLQFQHNLSNL 60
DB 109 TVWGGQFQIDGRSARGGQSANDAYAKALNSGSKSEALNVIRELVKDFVLQFQHNLSNL 168
QY 61 DRIFDKTPEP 70
DB 169 DRIFQPPAP 178

RESULT 4
VAL1_CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eady P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
R Nucleic Acids Res. 18:197-198(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X17095; CAA34953.1; -.
DR F1R; S07594; S07594.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16BB0CB2D5E2C CRC64;

Query Match 64.2%; Score 230; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 1.3e-19;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGRGCGTSDNDAALAAASAAALQIIRKIPKYLQFQHNLSNL 60
DB 109 TVWGGQFQIDGRSARGGQSANDAYAKALNSGSKSEALNVIRELVKDFVLQFQHNLSNL 168
QY 61 DRIFDKTPEP 70
DB 169 DRIFQPPAP 178
```

DR	EMBL; X15983; -; NOT_ANNOTATED_CDS.
DR	PIR; A36214; QOCVWL.
DR	InterPro; IPR001191; Gemini_AL1.
DR	Pfam; PF00799; Gemini_AL1; 1.
DR	PRINTS; PR00227; GEMCOATL1.
DR	ProDom; PD000736; Gemini_AL1; 1.
KW	ATP-binding.
FT	NP_BIND 221 228 ATP (POTENTIAL).
DR	SEQUENCE 355 AA; 40257 MW; 16A2C8A63251E95 CRC64;
DR	Query Match 60.6%; Score 217; DB 1; Length 355;
DR	Best Local Similarity 58.6%; Pred. No. 4.3e-18;
DR	Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
DR	1 TLWGFEQVDGRSARGCGTSDNDAARAALASSAAALQIIREKIPKYLQFQHNLSNL 60
DR	110 TAEWGFQIDGRSARGCGQTANDSYAKALNAGDVQSALNLIKKEQPKDYVLQNHNRSL 169
DR	61 DRIFDKTPEP 70
DR	170 ERIFAKAPEP 179
DR	RESULT 7
DR	ID VAL1 PHUV STANDARD; PRT; 349 AA.
DR	AC Q06923; 01-JUN-1994 (Rel. 29, Created)
DR	DT 01-JUN-1994 (Rel. 29, Last sequence update)
DR	DT 01-JUN-1994 (Rel. 29, Last annotation update)
DR	DE AL1 protein.
DR	GN AL1.
DR	OS Pepper huasteco virus (PHV).
DR	OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
DR	OX NCBI_TaxID=28349;
DR	RN [1]
DR	RP SEQUENCE FROM N.A.
DR	RX MEDLINE=94015007; PubMed=8409944;
DR	RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
DR	RA Rivera-Bustamante R.F.;
DR	RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
DR	RT comparison with bipartite geminiviruses.";
DR	RT J. Gen. Virol. 74:2225-2231(1993).
DR	CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR	CC This SWISS-PROT entry is copyright. It is produced through a collaboration
DR	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
DR	CC the European Bioinformatics Institute. There are no restrictions on its
DR	CC use by non-profit institutions as long as its content is in no way
DR	CC modified and this statement is not removed. Usage by and for commercial
DR	CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
DR	CC or send an email to license@isb-sib.ch).
DR	CC EMBL; X70418; CAA49856.1; -.
DR	PIR; JQ2300; JQ2300.
DR	PIR; S31875; S31875.
DR	InterPro; IPR001191; Gemini_AL1.
DR	Pfam; PF00799; Gemini_AL1; 1.
DR	PRINTS; PR00227; GEMCOATL1.
DR	ProDom; PD000736; Gemini_AL1; 1.
KW	ATP-binding.
FT	NP_BIND 221 228 ATP (BY SIMILARITY).
DR	SEQUENCE 349 AA; 39722 MW; D5F4E76CD56370F4 CRC64;
DR	Query Match 60.3%; Score 216; DB 1; Length 349;
DR	Best Local Similarity 58.6%; Pred. No. 5.5e-18;
DR	Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
DR	1 TLWGFEQVDGRSARGCGTSDNDAARAALASSAAALQIIREKIPKYLQFQHNLSNL 60
DR	110 TVRWGFQIDGRSARGCGQSDNTYAKALNSAEEALQITKEEQPHFFLQFHNVSNA 169
DR	61 DRIFDKTPEP 70


```

Query Match      59.8%; Score 214; DB 1; Length 361;
Best Local Similarity 55.7%; Pred. No. 9.8e-18;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDCRSARGGCGQTSNDAAAALAAASSAAAAAQIIREKIPEKYLQFHHNLSNL 60
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 110 TIWGDFFDGRSARGGQSSANDSYAKALNAGSVQSALAVLRERQDFVLQNHINRSL 169
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 11
VAL1_TYLCM
ID VAL1_TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (Cl protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92107660; PubMed=1840676;
RA Khayr-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a
RT whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X61153; CAA43466.1; -.
DR PIR; S22593; S22593.
DR PDB; 1L2M; 18-SEP-02.
DR PDB; 1L51; 18-SEP-02.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding; 3D-structure.
FT NP BIND 220 227
FT SEQUENCE 359 AA; 40733 MW; 9717B4A07C93EFA7 CRC64;

Query Match      59.2%; Score 212; DB 1; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.7e-17;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 2 LVWGEFQVDCRSARGGCGQTSNDAAAALAAASSAAAAAQIIREKIPEKYLQFHHNLSNLD 61
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 111 LEWGTFFQDGRSARGGQTDANDAYAKINAGSKSQALDVIKELAPRDYVLHFRHNSNLD 170
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 62 RIFDKTPEP 70
Db 171 KVQFQVPEP 179
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 12
VAL1_BCTV
ID VAL1_BCTV STANDARD; PRT; 358 AA.
AC P14991;
DT 01-APR-1990 (Rel. 14, Created)

```

```

DR EMBL; X15656; CAA33688.1; -.
DR PIR; D40779; QQCVC1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding. 219 226 ATP (POTENTIAL).
FT NP_BIND 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match
Best Local Similarity 53.1%; Score 190; DB 1; Length 357;
Matches 37; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 4 WGEFQVDSRGCGQTSNDAAALAAASSAAALQIIRKIPKYLFOFHNLNSLDRI 63
Db 111 FGVSDIGRSARGGQSQSANDAYAEALNSGSKSEALNLKAPKDYILQFHNLSSLDRI 170

QY 64 F 64
Db 171 F 171

RESULT 14
VAL1 SLCV STANDARD; PRT; 347 AA.
ID VAL1 SLCV
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI TaxID=10829;
RN [1]_
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G., Lazdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic components of a bipartite squash leaf curl geminivirus with a broad host range phenotype.";
RT Virology 180:58-69(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M38183; AAC32410.1; ALT_INIT.
CC PIR; C36785; QQCVS1.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding. 218 225 ATP (POTENTIAL).
FT NP_BIND 347 AA; 39110 MW; AFAABDDE122110E CRC64;
SQ SEQUENCE 347 AA; 39110 MW; AFAABDDE122110E CRC64;

Query Match
Best Local Similarity 32.1%; Score 115; DB 1; Length 347;
Matches 24; Conservative 14; Mismatches 24; Indels 4; Gaps 1;

QY 5 GEFQVDSRGCGQTSNDAAALAAASSAAALQIIRKIPKYLFOFHNLNSLDRI 64
Db 116 GQYKVSQ----GSKSNKDDVYHNAVNSAGSAGEALDIKAGDPKTFIVYHNLNANVERLF 171

QY 65 DKTPEP 70
Db 172 QKPEP 177

```

RESULT 15

SP8H HUMAN

```

ID Q8IXZ3; Q96MJ1;
AC Q8IXZ3; Q96MJ1;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical sp-like zinc finger protein MGC41921/FLJ322295.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Prostate;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuno Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
[2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M., Uedlin T.B., Toehlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc Natl Acad Sci U S A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8IXZ3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8IXZ3-2; Sequence=VSP_007441;
CC -!- SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER
CC PROTEINS.
CC -!- SIMILARITY: Contains 3 C2H2-type zinc fingers.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-19 is the initiator.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AK056857; BAB71297.1; -.
CC EMBL; BC038669; AAH38669.1; -.

```

DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF00096; zf-C2H2; 3.
DR ProDom: PD000003; Znf_C2H2; 1.
DR SMART: SM00355; Znf_C2H2; 3.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 3.
KW Hypothetical protein; Nuclear protein; Zinc-finger; Metal-binding;
KW DNA-binding; Repeat; Alternative splicing.
FT DOMAIN 29 132 SER-RICH.
FT DOMAIN 86 99 ALA-RICH.
FT ZN_FING 332 356 C2H2-TYPE 1.
FT ZN_FING 362 386 C2H2-TYPE 2.
FT ZN_FING 392 414 C2H2-TYPE 3.
FT VARSPLIC 111 124 Missing (in isoform 2).
FT /FTid=VSP_007441.
FT CONFLICT 406 406 R -> H (IN REF. 1).
SQ SEQUENCE 466 AA; 47079 MW; AD23BC6C0A9D5401 CRC64;

Query Match 19.7%; Score 70.5; DB 1; Length 466;
Best Local Similarity 59.4%; Pred. No. 1;
Matches 19; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

Qy 7 FQVDGRSARGCQTSNDAAAAAALAAASAAAAAL 38
Db 72 FGVSGASRNGG---SSSAAAAAAAAAAAAAAAAAL 100

Search completed: December 23, 2003, 08:57:37
Job time : 7.7778 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 25.3333 Seconds
(without alignments)
713.040 Million cell updates/sec

Title: US-09-289-346B-3
Perfect score: 358
Sequence: 1 TLVWGFQVDRSGRGCGQT.....FQFHNLSNLDRIEDKTPPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 23.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_ricent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	293	81.8	351	12 Q91R10	Q91R10 tomato seve
2	291	81.3	352	12 Q9E000	Q9E000 tomato rugo
3	284	79.3	232	12 Q8QV3	Q8QV3 tomato chlo
4	276	77.1	226	12 Q09727	Q09727 leonurus mo
5	271	75.7	314	12 Q9ELT8	Q9ELT8 sweet potat
6	271	75.7	364	12 Q9QS55	Q9QS55 sweet potat
7	264	73.7	226	12 Q9WHF6	Q9WHF6 tomato mild
8	263	73.5	359	12 Q91M88	Q91M88 tobacco lea
9	263	73.5	359	12 Q8JVB8	Q8JVB8 tomato curl
10	262	73.2	361	12 Q67574	Q67574 bean golden
11	260	72.6	149	12 P88975	P88975 macroptiliu
12	260	72.6	225	12 Q9QDB1	Q9QDB1 cowpea gold
13	260	72.6	233	12 Q9YLA4	Q9YLA4 macroptiliu
14	259	72.3	185	12 Q98693	Q98693 sida golden
15	257	71.8	360	12 Q8QMH4	Q8QMH4 sida mottle
16	255	71.2	361	12 Q8QVH0	Q8QVH0 ageratum en

17	253	70.7	235	12 Q8QPU4	Q8QPU4 tomato infe
18	252	70.4	208	12 Q8JLY3	Q8JLY3 potato yell
19	252	70.4	289	12 Q8JLY5	Q8JLY5 potato yell
20	251	70.1	190	12 Q9Z089	Q9Z089 tobacco lea
21	251	70.1	190	12 Q9Z084	Q9Z084 tobacco lea
22	251	70.1	223	12 Q8QPU7	Q8QPU7 tomato seve
23	250	69.8	190	12 Q9W827	Q9W827 tobacco lea
24	250	69.8	208	12 Q9Z0C0	Q9Z0C0 tobacco lea
25	250	69.8	208	12 Q9Z0C4	Q9Z0C4 tobacco lea
26	250	69.8	208	12 Q9Z0B8	Q9Z0B8 tobacco lea
27	249	69.6	208	12 Q9Z0A0	Q9Z0A0 tobacco lea
28	248	69.3	208	12 Q9Z0C6	Q9Z0C6 tobacco lea
29	248	69.3	361	12 Q8JMJ4	Q8JMJ4 potato yell
30	247	69.0	362	12 Q56816	Q56816 chayote mos
31	246	68.7	208	12 Q9Z0B6	Q9Z0B6 tobacco lea
32	246	68.7	364	12 Q8V5Z4	Q8V5Z4 ipomoea lea
33	245	68.4	203	12 Q9Z0E3	Q9Z0E3 tobacco lea
34	245	68.4	363	12 Q73577	Q73577 cotton leaf
35	244	68.2	359	12 Q8V380	Q8V380 east africa
36	244	68.2	362	12 Q8V016	Q8V016 cotton leaf
37	244	68.2	362	12 Q8V018	Q8V018 cotton leaf
38	244	68.2	362	12 Q8V618	Q8V618 cotton leaf
39	244	68.2	362	12 Q8V0H6	Q8V0H6 okra leaf c
40	244	68.2	362	12 Q9IN48	Q9IN48 okra enatio
41	243	67.9	234	12 Q39180	Q39180 geminivirid
42	242	67.6	231	12 Q96620	Q96620 african tom
43	242	67.6	353	12 Q72692	Q72692 beet curly
44	242	67.6	354	12 Q65438	Q65438 beet curly
45	242	67.6	359	12 Q9YZV4	Q9YZV4 tomato yell

ALIGNMENTS

RESULT 1
Q91R10 PRELIMINARY; PRT; 351 AA.
ID Q91R10
AC Q91R10; 2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DT 01-MAR-2003 (TREMREL. 23, Last annotation update)
DE Rep protein.
GN ACI
OS Tomato severe rugose virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=158463;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Minas Gerais;
RA Rezende W.L., Goulart L.R., Parreira K.S., Figueiredo J.E.F.;
RT "The full-length DNA-A nucleotide sequence of a novel tomato-infecting
RT begomovirus, tomato severe rugose virus, in Brazil."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029750; AAK50357.1; -
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1.1.
SQ SEQUENCE 351 AA; 40122 MW; 879937A4F873B6CF CRC64;

Query Match 81.8%; Score 293; DB 12; Length 351;
Best Local Similarity 78.6%; Pred. No. 4.6e-26;
Matches 55; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY	1	TLVWGFQVDRSGRGCGQTSDAAALAAASAAAALQIIREKIPKYLPOFHNLSNL	60
Db	111	TLVWGFQVDRSGRGCGQTSDAAALAAASAAAALQIIREKIPKYLPOFHNLSNL	170
QY	61	DRIFDKTPPEP 70	
Db	171	DRIFARPEP 180	

```

RESULT 2
Q9E000
ID Q9E000 PRELIMINARY; PRT; 352 AA.
AC Q9E000;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE Replication-associated protein.
GN AC1.
OS Tomato rugose mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=134599;
RN [1]
RP SEQUENCE FROM N.A.
RA Fernandes J.J., Fontes E.P.B., Brommonschenkel S.H., Carvalho M.G.,
RA Zambolim E.M., Zerbini F.M.;
RT "Molecular Cloning and Characterization of Tomato rugose mosaic virus
RT (TRMV), a Begomovirus Isolated from Tomatoes at Triangulo Mineiro,
RT Minas Gerais, Brazil.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF291705; AAG15546.1; -.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini AL1; 1.
SQ SEQUENCE 352 AA; 40012 MW; 47CD55838E24D613 CRC64;

Query Match 81.3%; Score 291; DB 12; Length 352;
Best Local Similarity 78.6%; Pred. No. 7.9e-26;
Matches 55; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQDGRSARGGQTSNDAAAALAAASSAAALQIIREKIPEKLFQFHNLSNL 60
Db 111 TLVWGEFQDGRSARGGQTSNDAAAALAAASSAAALQIIREKIPEKLFQFHNLSNL 170

QY 61 DRIFDKTPEP 70
Db 171 DRIFARAPEP 180

RESULT 3
Q8QPV3
ID Q8QPV3 PRELIMINARY; PRT; 232 AA.
AC Q8QPV3;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Tomato chlorotic vein virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172390;
RN [1]
RP SEQUENCE FROM N.A.
RA Ribeiro S.G., Ambrozecivius L.P., de Avila A.C., Calegario R.P.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049205; AAL82824.1; -.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; I.
DR ProDom; PD000736; Gemini AL1; 1.
FT NON_TER 232
SQ SEQUENCE 232 AA; 26319 MW; 254CASD040D35DDA CRC64;

Query Match 79.3%; Score 284; DB 12; Length 232;
Best Local Similarity 77.1%; Pred. No. 3.2e-25;
Matches 54; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQDGRSARGGQTSNDAAAALAAASSAAALQIIREKIPEKLFQFHNLSNL 60
Db 111 TLVWGEFQDGRSARGGQTSNDAAAALAAASSAAALQIIREKIPEKLFQFHNLSNL 170

RESULT 4
O09727
ID O09727 PRELIMINARY; PRT; 226 AA.
AC O09727;
DT 01-JUL-1997 (TREMELrel. 04, Created)
DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN REP.
OS Leonurus mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=58177;
RN [1]
RP SEQUENCE FROM N.A.
RA Faria J.C., Maxwell D.P.;
RT "Variability in geminivirus associated with Phaseolus vulgaris in
RT Brazil.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U92532; AAB51157.1; -.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini AL1; 1.
FT NON_TER 226
SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;

Query Match 77.1%; Score 276; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 2.7e-24;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQDGRSARGGQTSNDAAAALAAASSAAALQIIREKIPEKLFQFHNLSNL 60
Db 111 TLVWGEFQDGRSARGGQTSNDAAAALAAASSAAALQIIREKIPEKLFQFHNLSNL 170

QY 61 DRIFDKTPEP 70
Db 171 DRIFAKAPEP 180

RESULT 5
Q9ELT8
ID Q9ELT8 PRELIMINARY; PRT; 314 AA.
AC Q9ELT8;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Replication association protein.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288227; AAG01006.1; -.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; I.
DR PRINTS; PR00227; GEMCOATALL.

```


DE Cl protein.
 OS Tomato curly stunt virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=128941;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pieterse G., Idris A.M., Kruger K., Brown J.K.;
 RT "Tomato curly stunt virus, a new Begomovirus of tomato within TYLCV-Is
 RT cluster in South Africa."
 RL Plant Dis. 84:810-810(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pieterse G., Idris A.M., Kruger K., Brown J.K.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF261885; AAM80474.1; -;
 DR InterPro; IPR001191; Gemini_AL1.
 DR Pfam; PF00799; Gemini_AL1; 1.
 DR PRINTS; PR00227; GEMCOATL1.
 DR ProDom; PD000736; Gemini_AL1; 1.
 SQ SEQUENCE 359 AA; 40715 MW; 751159837A87FDCC CRC64;
 Query Match 73.5%; Score 263; DB 12; Length 359;
 Best Local Similarity 70.0%; Pred. No. 1.6e-22;
 Matches 49; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDSARGCGQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNLL 60
 Db 110 TLEWGFQVDSARGCGQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNLL 60
 QY 61 DRIFDKTPEP 70
 Db 170 DRIFQAPPEP 179
 RESULT 10
 Q67574
 ID Q67574 PRELIMINARY; PRT; 361 AA.
 AC Q67574;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE Putative replicative protein.
 GN AL1.
 OS Bean golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
 RA Morales F.J., Maxwell D.P.;
 RT "Cloning of the complete DNA genomes of four bean-infecting
 RT geminiviruses and determining their infectivity by electric discharge
 RT particle acceleration."
 RL Phytopathology 81:980-985(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
 RA Morales F.J., Maxwell D.P.;
 RT "Differentiation of bean-infecting geminiviruses by nucleic acid
 RT hybridization probes and aspects of bean golden mosaic in Brazil."
 RL Plant Dis. 75:336-342(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
 RT "Genetic diversity in geminiviruses causing bean golden mosaic
 RT disease: The nucleotide sequence of the infectious cloned DNA
 RT components of a Brazilian isolate of bean golden mosaic geminivirus."
 RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M88686; AAA46312.1; -;
 DR InterPro; IPR001191; Gemini_AL1.
 DR Pfam; PF00799; Gemini_AL1; 1.
 DR PRINTS; PR00227; GEMCOATL1.
 DR ProDom; PD000736; Gemini_AL1; 1.

SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;
 Query Match 73.2%; Score 262; DB 12; Length 361;
 Best Local Similarity 73.1%; Pred. No. 2.1e-22;
 Matches 49; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
 QY 4 WGSFQVDSARGCGQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNLL 63
 Db 113 WGHFQVDSARGCGQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNLL 172
 QY 64 DRFKTPEP 70
 Db 173 FTKAPDP 179
 RESULT 11
 P88975
 ID P88975 PRELIMINARY; PRT; 149 AA.
 AC P88975;
 DT 01-MAY-1997 (T-EMBLrel. 03, Created)
 DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
 DT 01-MAY-2003 (T-EMBLrel. 23, Last annotation update)
 DE Replication-associated protein (Fragment).
 GN ACl.
 OS Macrotetium golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=51676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Jamaican;
 RA Roye M.E.;
 RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
 DR EMBL; U75278; AAB36919.1; -;
 DR InterPro; IPR001191; Gemini_AL1.
 DR Pfam; PF00799; Gemini_AL1; 1.
 DR PRINTS; PR00227; GEMCOATL1.
 DR ProDom; PD000736; Gemini_AL1; 1.
 FT NON TER 1 149
 FT NON TER 149 149
 SQ SEQUENCE 149 AA; 16785 MW; E4CF5EDD4C9CD508 CRC64;
 Query Match 72.6%; Score 260; DB 12; Length 149;
 Best Local Similarity 68.6%; Pred. No. 1.3e-22;
 Matches 48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDSARGCGQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNLL 60
 Db 52 TTEWGFQVDSARGCGQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNLL 111
 QY 61 DRIFDKTPEP 70
 Db 112 DRIFMKDPEP 121
 RESULT 12
 Q9QDB1
 ID Q9QDB1 PRELIMINARY; PRT; 225 AA.
 AC Q9QDB1;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Replication associated protein (Fragment).
 GN REP.
 OS Cowpea golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=69263;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGMV-BR;
 RA Faria J.C.;
 RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
 RT Brazil."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

Qy 64 PDKTPEP 70
| | | |
Db 174 FLKAPPEP 180

Search completed: December 23, 2003, 09:03:35
Job time : 26.3333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds
(without alignments)
340.128 Million cell updates/sec

Title: US-09-289-346B-4
Perfect score: 361
Sequence: 1 TLVWSEFQVDSARGCQT.....FQFHNLSNLDIFDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361	100.0	70	21	AA18680
2	346	95.8	70	21	AA18677
3	346	95.8	356	21	AA18687
4	338	93.6	70	21	AA18685
5	335	92.8	70	21	AA18688
6	334	92.5	70	21	AA18692
7	332	92.0	70	21	AA18684
8	332	92.0	70	21	AA18690
9	331	91.7	70	21	AA18678

10	331	91.7	70	21	AA18686	Mutant peptide der
11	330	91.4	70	21	AA18689	Mutant peptide der
12	328	90.9	70	21	AA18691	Mutant peptide der
13	325	90.0	70	21	AA18681	Mutant peptide der
14	324	89.8	70	21	AA18683	Mutant peptide der
15	322	89.2	70	21	AA18682	Mutant peptide der
16	314	87.0	70	21	AA18679	Mutant peptide der
17	222	61.5	359	17	AA18680	Sardinian tomato y
18	222	61.5	359	17	AA18687	Sardinian tomato y
19	219	60.7	353	18	AA18681	Bean golden mosaic
20	219	60.7	353	18	AA18683	Bean golden mosaic
21	219	60.7	353	18	AA18682	Bean golden mosaic
22	219	60.7	353	18	AA18683	Bean golden mosaic
23	219	60.7	353	18	AA18683	Bean golden mosaic
24	219	60.7	353	18	AA18683	Bean golden mosaic
25	217	60.1	353	8	AA18680	ORF 4 gene product
26	214	59.3	361	18	AA18683	Tomato mottle viru
27	214	59.3	361	18	AA18683	Tomato mottle viru
28	214	59.3	361	18	AA18683	Tomato mottle viru
29	214	59.3	361	18	AA18683	Tomato mottle viru
30	205.5	56.9	50	23	AA18683	Retinoblastoma-bin
31	203.5	56.4	361	8	AA18683	Product of ORF 4 f
32	200	55.4	357	18	AA18683	Tomato yellow leaf
33	200	55.4	357	18	AA18683	Tomato yellow leaf
34	200	55.4	357	18	AA18683	Tomato yellow leaf
35	198	54.8	362	19	AA18683	Tobacco leaf curl
36	192	53.2	357	18	AA18683	Tomato yellow leaf
37	104	28.8	142	24	AA18683	Tomato yellow leaf
38	65.5	18.1	512	19	AA18683	HIV-1 strain YBF30
39	63.5	17.6	665	22	AA18683	Drosophila melanog
40	61.5	17.0	183	21	AA18683	Arabidopsis thalia
41	61.5	17.0	299	18	AA18683	H. pylori ORF 02ae
42	61.5	17.0	1203	21	AA18683	Candida albicans C
43	61.5	17.0	1203	21	AA18683	Amino acid sequenc
44	61	16.9	483	22	AA18683	C glutamicum prote
45	60.5	16.8	131	18	AA18683	Tomato mottle viru

ALIGNMENTS

RESULT 1
AA18680
ID AA18680 standard; peptide; 70 AA.
XX AA18680;
AC AA18680;
DT 22-JAN-2001 (first entry)
XX

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW ribosome binding region; resistance; geminivirus infection.
XX

OS Synthetic.
OS Tomato golden mosaic virus.

PH Key Location/Qualifiers
FT Misc-difference 42 /note= "wild type residue replaced with Ala"
FT Misc-difference 43 /note= "wild type residue replaced with Ala"
FT Misc-difference 44 /note= "wild type residue replaced with Ala"
XX| XX | WO2000054573-A1. |
XX	21-SRP-2000.
XX	15-MAR-2000; 2000WO-US06759.
XX	18-MAR-1999; 99US-0125004.
XX	09-APR-1999; 99US-0289346.

XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX XX
PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT -
XX XX
PS Claim 52; Page 43-44; 73pp; English.
XX XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX XX
SQ Sequence 70 AA;
Query Match 100.0%; Score 361; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.6e-39;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDRSGRGCGTSDNDAAEALNASSKEEALQIIAAIPEKYLFOFHNLSNL 60
DB 1 TLVWGEFQVDRSGRGCGTSDNDAAEALNASSKEEALQIIAAIPEKYLFOFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 2
AAB18677
ID AAB18677 standard; peptide; 70 AA.
XX AAB18677;
XX XX
DT 22-JAN-2001 (first entry)
XX XX
DE Peptide fragment from Rep protein of TGMV (amino acids 110-179).
XX XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW ribosome binding region; resistance; geminivirus infection.
XX OS Tomato golden mosaic virus.
XX PN WO200054573-A1.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-US06759.
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
PT Transgenic plants with increased resistance to geminivirus infection

XX PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT -
XX XX
PS Disclosure; Page 18; 73pp; English.
XX XX
CC The present sequence is derived from a geminivirus replication (Rep)
CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
CC with other viral and host proteins. Mutants of the AL1 protein are used
CC to produce transgenic plants. The mutation in AL1 is present in a
CC ribosome binding region, and expression of mutant AL1 protein imparts
CC increased resistance to geminivirus infection in the plant. Mutant AL1
CC proteins are useful for producing plants having increased resistance or
CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
CC beet curly top virus.
XX XX
SQ Sequence 70 AA;
Query Match 95.8%; Score 346; DB 21; Length 70;
Best Local Similarity 95.7%; Pred. No. 1.5e-37;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDRSGRGCGTSDNDAAEALNASSKEEALQIIAAIPEKYLFOFHNLSNL 60
DB 1 TLVWGEFQVDRSGRGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 3
AAB18687
ID AAB18687 standard; peptide; 356 AA.
XX AAB18687;
XX XX
DT 22-JAN-2001 (first entry)
XX XX
DE Amino acid sequence of a geminivirus replication protein of TGMV.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW ribosome binding region; resistance; geminivirus infection.
XX OS Tomato golden mosaic virus.
XX XX
FH Key Location/Qualifiers
FT FT Misc-difference 354
FT FT /note= "unspecified amino acid"
PN WO200054573-A1.
XX XX
PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-US06759.
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
PT Transgenic plants with increased resistance to geminivirus infection

comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant AL1 protein with a mutation in the Rb binding region

Disclosure, Page 47-48; 73pp; English.

The present sequence represents a geminivirus replication (Rep) protein, which is also known as AL1. AL1 binds double-stranded DNA, catalyzes cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the AL1 protein are used to produce transgenic plants. The mutation in AL1 is present in a ribosome binding region, and expression of mutant AL1 protein imparts increased resistance to geminivirus infection in the plant. Mutant AL1 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian cassava mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, yellow mosaic virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

Query Match 95.8%; Score 346; DB 21; Length 356;
Best Local Similarity 95.7%; Pred. No. 1.2e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGQTSNDAAAEALNASSKEEALQIIIAAIPKYLFPQHNLNSNL 60
DB 110 TLVWGEFQVDSARGCGQTSNDAAAEALNASSKEEALQIIIREKIPEKYLFPQHNLNSNL 169
QY 61 DRIFDKTPEP 70
DB 170 DRIFDKTPEP 179

RESULT 4
AAB18685
ID AAB18685 standard; peptide; 70 AA.

AC AAB18685;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW ribosome binding region; resistance; geminivirus infection.

OS Synthetic.

OS Tomato golden mosaic virus.

PH Key Location/Qualifiers

FT Misc-difference 10 /note= "wild type residue replaced with Ala"

FT WO200054573-A1.

PN 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

Transgenic plants with increased resistance to geminivirus infection comprise a nucleic acid construct containing a nucleic acid sequence

encoding a mutant AL1 protein with a mutation in the Rb binding region

Claim 53; Page 46; 73pp; English.

The present sequence represents a mutant peptide, derived from a geminivirus replication (Rep) protein, also known as AL1. AL1 binds double-stranded DNA, catalyzes cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the AL1 protein are used to produce transgenic plants. The mutation in AL1 is present in a ribosome binding region, and expression of mutant AL1 protein imparts increased resistance to geminivirus infection in the plant. Mutant AL1 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian cassava mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, yellow mosaic virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

SQ Sequence 70 AA;

Query Match 93.6%; Score 338; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 1.6e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGQTSNDAAAEALNASSKEEALQIIIAAIPKYLFPQHNLNSNL 60

DB 1 TLVWGEFQVDSARGCGQTSNDAAAEALNASSKEEALQIIIREKIPEKYLFPQHNLNSNL 60

QY 61 DRIFDKTPEP 70

DB 61 DRIFDKTPEP 70

RESULT 5

AAB18688

ID AAB18688 standard; peptide; 70 AA.

AC AAB18688;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

KW ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

OS Tomato golden mosaic virus.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 19 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT WO200054573-A1.

PN 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence
 FT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX
 PS Disclosure; Page 48; 73pp; English.

CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;
 SQ Query Match 92.8%; Score 335; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 4e-36;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGCQTNDAAAEALNASSKEEALQIIAAIPKYLQFPHNLSNL 60
 DB 1 TLVWGEFQVDSRGSGCAASNDAAAEALNASSKEEALQIIREKIPKYLQFPHNLSNL 60

QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70

RESULT 6
 AAB18692
 ID AAB18692 standard; peptide; 70 AA.

AC AAB18692;
 XX
 XX 22-JAN-2001 (first entry)
 DT
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 DE
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 66 /note= "wild type residue replaced with Ala"
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"
 FT
 XX
 XX WO200054573-Al.

XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI
 XX WPI; 2000-618851/59.
 XX
 XX

PT Transgenic plants with increased resistance to geminivirus infection
 FT comprise a nucleic acid construct containing a nucleic acid sequence
 FT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX
 PS Disclosure; Page 50; 73pp; English.

CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;

Query Match 92.5%; Score 334; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 5.5e-36;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGCQTNDAAAEALNASSKEEALQIIAAIPKYLQFPHNLSNL 60
 DB 1 TLVWGEFQVDSRGSGCQTNDAAAEALNASSKEEALQIIREKIPKYLQFPHNLSNL 60

QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70

RESULT 7
 AAB18684
 ID AAB18684 standard; peptide; 70 AA.

AC AAB18684;
 VX
 XX 22-JAN-2001 (first entry)
 DT
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 DE
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 7 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"
 FT
 XX
 XX WO200054573-Al.

XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI
 XX WPI; 2000-618851/59.
 XX
 XX

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX
 PS Claim 52; Page 45; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 92.0%; Score 332; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 1e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDSARGGCGTSDNDAARALNASSKEALQIIAAIPEKYLQFHNLSNL 60
 DB 1 TLVWGEAAVDGSRAGGCGTSDNDAARALNASSKEALQIIREKIPEKYLQFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 8
 AAB18690
 ID AAB18690 standard; peptide; 70 AA.
 AC AAB18690;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 27 /note= "wild type residue replaced with Ala"
 FT Misc-difference 30 /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-A1.
 FN
 XX 21-SEP-2000.
 PD
 XX 15-MAR-2000; 2000WO-US06759.
 PF
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hanley-Bowdoin L, Orozco EM, Kong L;
 XX

DR WPI; 2000-618851/59.
 XX
 PT Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX
 PS Disclosure; Page 49; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 92.0%; Score 332; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 1e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDSARGGCGTSDNDAARALNASSKEALQIIAAIPEKYLQFHNLSNL 60
 DB 1 TLVWGEAAVDGSRAGGCGTSDNDAARALNASSKEALQIIREKIPEKYLQFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 9
 AAB18678
 ID AAB18678 standard; peptide; 70 AA.
 AC AAB18678;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 12 /note= "wild type residue replaced with Ala"
 FT Misc-difference 13 /note= "wild type residue replaced with Ala"
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-A1.
 FN
 XX 21-SEP-2000.
 PD
 XX 15-MAR-2000; 2000WO-US06759.
 PF
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.

```

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT Transgenic plants with increased resistance to geminivirus infection
XX FT comprise a nucleic acid construct containing a nucleic acid sequence
XX FT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PS
XX PS Claim 53; Page 42-43; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 91.7%; Score 331; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.3e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIIAAAIPEKYLQFHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 10
AAB18686
ID AAB18686 standard; peptide; 70 AA.
AC AAB18686;
DT 22-JAN-2001 (first entry)
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX Key Location/Qualifiers
FT Misc-difference 24 /note= "wild type residue replaced with Leu"
FT Misc-difference 25 /note= "wild type residue replaced with Leu"
FT Misc-difference 26 /note= "wild type residue replaced with Leu"
XX WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.

```

```

PR 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT Transgenic plants with increased resistance to geminivirus infection
XX FT comprise a nucleic acid construct containing a nucleic acid sequence
XX FT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PS
XX PS Claim 53; Page 46; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 91.7%; Score 331; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.3e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIIAAAIPEKYLQFHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTNDLLLEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 11
AAB18689
ID AAB18689 standard; peptide; 70 AA.
AC AAB18689;
DT 22-JAN-2001 (first entry)
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX Key Location/Qualifiers
FT Misc-difference 22 /note= "wild type residue replaced with Ala"
FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX

```

```

PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
PA (UYN-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant ALI protein with a mutation in the Rb binding region
XX
XX Disclosure; Page 48-49; 73pp; English.
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as ALI. ALI binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the ALI
CC protein are used to produce transgenic plants. The mutation in ALI is
CC present in a ribosome binding region, and expression of mutant ALI
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant ALI proteins are useful for producing plants having
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 91.4%; Score 330; DB 21; Length 70;
XX Best Local Similarity 92.9%; Pred. No. 1.8e-35;
XX Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGFQVDSARGGCTSDNDAAEALNASSKEALQITAAIPKYLQFHNLSNL 60
DB 1 TLVWGFQVDSARGGCTSDNDAAEALNASSKEALQITAAIPKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 12
AAB18691
ID AAB18691 standard; peptide; 70 AA.
XX AAB18691;
AC AAB18691;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.
XX Geminivirus; replication protein; Rep protein; ALI; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX Misc-difference 34 /note= "wild type residue replaced with Ala"
XX Misc-difference 35 /note= "wild type residue replaced with Ala"
XX Misc-difference 36 /note= "wild type residue replaced with Ala"
XX Misc-difference 36 /note= "wild type residue replaced with Ala"
XX WO2000054573-A1.
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
PA (UYN-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant ALI protein with a mutation in the Rb binding region
XX
XX Disclosure; Page 49; 73pp; English.
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as ALI. ALI binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the ALI
CC protein are used to produce transgenic plants. The mutation in ALI is
CC present in a ribosome binding region, and expression of mutant ALI
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant ALI proteins are useful for producing plants having
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 90.9%; Score 328; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 3.3e-35;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 TLVWGFQVDSARGGCTSDNDAAEALNASSKEALQITAAIPKYLQFHNLSNL 60
DB 1 TLVWGFQVDSARGGCTSDNDAAEALNASSKEALQITAAIPKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 13
AAB18681
ID AAB18681 standard; peptide; 70 AA.
XX AAB18681;
AC AAB18681;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.
XX Geminivirus; replication protein; Rep protein; ALI; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX Misc-difference 47 /note= "wild type residue replaced with Ala"
XX Misc-difference 48 /note= "wild type residue replaced with Ala"
XX Misc-difference 49 /note= "wild type residue replaced with Ala"
XX

```


PN WO200054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX Claim 52; Page 44; 73pp; English.
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA;
 SQ Query Match 90.0%; Score 325; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 8.3e-35;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 TLVWGEFQVDCRSARGCGQTSNDAAAEALNASSKEEALQIIAAAIPEKYLQFPHNLNSNL 60
 Db 1 TLVWGEFQVDCRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPAAALQFPHNLNSNL 60
 Qy 61 DRIFDKTPEP 70
 Db 61 DRIFDKTPEP 70
 RESULT 14
 AAB18683
 ID AAB18683 standard; peptide; 70 AA.
 AC AAB18683;
 XX 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 PH Misc-difference 59 /note= "wild type residue replaced with Ala"
 FT Misc-difference 61 /note= "wild type residue replaced with Ala"

FT Misc-difference 62 /note= "wild type residue replaced with Ala"
 FT XX WO200054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX Claim 53; Page 45; 73pp; English.
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA;
 SQ Query Match 89.8%; Score 324; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 1.1e-34;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 TLVWGEFQVDCRSARGCGQTSNDAAAEALNASSKEEALQIIAAAIPEKYLQFPHNLNSNL 60
 Db 1 TLVWGEFQVDCRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPKYLQFPHNLNSAL 60
 Qy 61 DRIFDKTPEP 70
 Db 61 AAFDKTPEP 70
 RESULT 15
 AAB18682
 ID AAB18682 standard; peptide; 70 AA.
 AC AAB18682;
 XX 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 PH Misc-difference 52

```

FT      /note= "wild type residue replaced with Ala"
FT Misc-difference 54
FT      /note= "wild type residue replaced with Ala"
FT Misc-difference 55
FT      /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX PD 21-SEP-2000.
XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX
XX (UYN-) UNIV NORTH CAROLINA STATE.
XX
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WP1; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant All protein with a mutation in the Rb binding region
XX
XX Claim 53; Page 44-45; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as All. All binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the All
XX protein are used to produce transgenic plants. The mutation in All is
XX present in a ribosome binding region, and expression of mutant All
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant All proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX SQ Sequence 70 AA;
XX
XX Query Match 89.2%; Score 322; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 2e-34;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 TLVWGGEFQVDSARGGCTNSDAAAEALNASSKEEALQITAAATPEKYLFEHNLNSNL 60
XX   |||||||
XX Db 1 TLVWGGEFQVDSARGGCTNSDAAAEALNASSKEEALQITAAATPEKYLFEHNLNSNL 60
XX   |||||||
XX QY 61 DRIFDKTPEP 70
XX   |||||||
XX Db 61 DRIFDKTPEP 70

```

Search completed: December 23, 2003, 08:56:29
 Job time : 32.6667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 11.6667 Seconds
(without alignments)
253.865 Million cell updates/sec

Title: US-09-289-346B-4

Perfect score: 361

Sequence: 1 TLVWGEFQVDSRGSGCQT.....FQPHNLNLDRIKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222	61.5	359	3	US-08-809-103B-2
2	222	61.5	359	3	US-08-809-103B-4
3	222	61.5	359	3	US-08-809-103B-6
4	222	61.5	359	3	US-08-809-103B-8
5	219	60.7	353	3	US-08-838-151A-44
6	219	60.7	353	3	US-08-838-151A-46
7	219	60.7	353	3	US-08-838-151A-49
8	219	60.7	353	3	US-08-838-151A-52
9	219	60.7	353	3	US-08-838-151A-55
10	214	59.3	361	3	US-08-838-151A-2
11	214	59.3	361	3	US-08-838-151A-4
12	214	59.3	361	3	US-08-838-151A-6
13	214	59.3	361	3	US-08-838-151A-8
14	200	55.4	357	3	US-08-838-151A-24
15	200	55.4	357	3	US-08-838-151A-27
16	200	55.4	357	3	US-08-838-151A-30
17	192	53.2	357	3	US-08-838-151A-20
18	65.5	18.1	512	4	US-09-319-588C-4
19	61.5	17.0	1203	4	US-09-351-200-2
20	60.5	16.8	131	3	US-08-838-151A-14
21	60.5	16.8	334	6	5290690-11
22	59.5	16.5	244	4	US-09-328-352-4541
23	58.5	16.2	356	1	US-08-781-582-1
24	58.5	16.2	426	4	US-09-252-991A-20262
25	57	15.8	602	2	US-08-419-652-6
26	57	15.8	771	1	US-07-923-976-6
27	57	15.8	783	6	5422248-2

28 57 15.8 836 1 US-07-923-976-4
29 57 15.8 863 1 US-07-923-976-8
30 56.5 15.7 242 4 US-09-252-991A-18664
31 56.5 15.7 606 4 US-09-252-991A-19545
32 56 15.5 1298 4 US-09-252-991A-30579
33 55.5 15.4 299 4 US-09-336-115C-24
34 55.5 15.4 724 4 US-09-252-991A-30884
35 55 15.2 783 6 5231168-2
36 54.5 15.1 258 3 US-08-251-645-5
37 54.5 15.1 1713 3 US-08-600-982-24
38 54.5 15.1 1713 5 PCT-US94-10261A-24
39 54 15.0 111 4 US-09-732-210-713
40 54 15.0 188 4 US-09-328-352-7291
41 54 15.0 271 1 US-08-276-919-10
42 54 15.0 271 1 US-08-776-088-13
43 54 15.0 271 5 PCT-US95-09145A-13
44 54 15.0 274 1 US-08-776-088-15
45 54 15.0 274 5 PCT-US95-09145A-15

ALIGNMENTS

RESULT 1

US-08-809-103B-2

; Sequence 2, Application US/08809103B

; Patent No. 6133505

; GENERAL INFORMATION:

; APPLICANT: GRONENBORN, Bruno

; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT

; NUMBER OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSER: YOUNG & THOMPSON

; STREET: 745 South 23rd Street

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/809,103B

; FILING DATE: 17-MAR-1997

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 94.11040

; FILING DATE: 15-SEP-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/FR95/01192

; FILING DATE: 15-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: PATCH, Andrew J.

; REGISTRATION NUMBER: 32,925

; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 521-2297

; TELEFAX: (703) 685-0573

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 359 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-809-103B-2

Query Match 61.5%; Score 222; DB 3; Length 359;

Best Local Similarity 58.0%; Pred. No. 5.3e-22;

Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGFEVDGSRAGGCGQTNDAAAEALNASSKEEALQITAAAIPEKYLQFPHNLSNLD 61
Db 111 LEWGTFTQIDGSRAGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170
Qy 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 2
US-08-809-103B-4
; Sequence 4, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; NAME: PATCH, Andrew J.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-4

Query Match 61.5%; Score 222; DB 3; Length 359;
Best Local Similarity 59.0%; Pred. No. 5.3e-22;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;
Qy 2 LVWGFEVDGSRAGGCGQTNDAAAEALNASSKEEALQITAAAIPEKYLQFPHNLSNLD 61
Db 111 LEWGTFTQIDGSRAGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170
Qy 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 3
US-08-809-103B-6
; Sequence 6, Application US/08809103B

; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; NAME: PATCH, Andrew J.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-6
Query Match 61.5%; Score 222; DB 3; Length 359;
Best Local Similarity 58.0%; Pred. No. 5.3e-22;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;
Qy 2 LVWGFEVDGSRAGGCGQTNDAAAEALNASSKEEALQITAAAIPEKYLQFPHNLSNLD 61
Db 111 LEWGTFTQIDGSRAGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170
Qy 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179
RESULT 4
US-08-809-103B-8
; Sequence 8, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,1038
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: US94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-1038-8

Query Match 61.5%; Score 222; DB 3; Length 359;
Best Local Similarity 58.0%; Pred. No. 5.3e-22;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRGARGGQTSNDAAAEALNASSKEEALQIIAAAIPEKYLQFHHNLSNLD 61
Db 111 LLEWTFQIDRGARGGQTDANDAYAKAINAGSKSQALDVIKELAPRDYVLHFHNSNLD 170

QY 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 5
US-08-838-151A-44
; Sequence 44, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiiviruses
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-44

Query Match 60.7%; Score 219; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 1.3e-21;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRGARGGQTSNDAAAEALNASSKEEALQIIAAAIPEKYLQFHHNLSNLD 60
Db 110 TIWEGFQVDRGARGGQSANDSYAKALNADSTESALTILKEQPKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 6
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiiviruses
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

Query Match 60.7%; Score 219; DB 3; Length 353;

```



```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-2

Query Match          59.3%; Score 214; DB 3; Length 361;
Best Local Similarity 55.7%; Pred. No. 6.6e-21;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0

QY      1 TLVWGEFQVDRSGRGCGQTSNDAAAEALNASSKEBALQIIAAAIPEKYLFQFHNLSNL 60
DDB     110 TIWGDQFIDRGARGGQGSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHMIRSL 169
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61 DRIFDKTPEP 70
DDB     170 ERIFAKAPEP 179
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-4

Query Match          59.3%; Score 214; DB 3; Length 361;
Best Local Similarity 55.7%; Pred. No. 6.6e-21;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0

QY      1 TLVWGEFQVDRSGRGCGQTSNDAAAEALNASSKEBALQIIAAAIPEKYLFQFHNLSNL 60
DB     110 TIWGDQFIDRGARGGQGSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHMIRSL 169

```

QY 61 DRIFDKTPEP 70
 :|||:|
 Db 170 ERIFAKAPEP 179

RESULT 12

US-08-838-151A-6
 ; Sequence 6, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; REFERENCE/DOCKET NUMBER: SVS3801P0260
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-616-5400
 ; TELEFAX: 312-616-5460
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 361 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-838-151A-6

Query Match 59.3%; Score 214; DB 3; Length 361;
 Best Local Similarity 55.7%; Pred. No. 6.6e-21;
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDRSARGGCGTNDAAAEALNASSKEALQITAAIPEKYLFPQFHNLSNL 60
 :|||:|
 Db 110 TTWGDGFDIGRSARGGQGSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHIRSNL 169
 :|||:|
 QY 61 DRIFDKTPEP 70
 :|||:|
 Db 170 ERIFAKAPEP 179

US-08-838-151A-6
 ; Sequence 6, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A

RESULT 13

US-08-838-151A-8
 ; Sequence 8, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

; TITLE OF INVENTION: Genes
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; REFERENCE/DOCKET NUMBER: SVS3801P0260
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-616-5400
 ; TELEFAX: 312-616-5460
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 361 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-838-151A-8

Query Match 59.3%; Score 214; DB 3; Length 361;
 Best Local Similarity 55.7%; Pred. No. 6.6e-21;
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDRSARGGCGTNDAAAEALNASSKEALQITAAIPEKYLFPQFHNLSNL 60
 :|||:|
 Db 110 TTWGDGFDIGRSARGGQGSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHIRSNL 169
 :|||:|
 QY 61 DRIFDKTPEP 70
 :|||:|
 Db 170 ERIFAKAPEP 179

RESULT 14

US-08-838-151A-24
 ; Sequence 24, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A


```
;
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-24

Query Match      55.4%; Score 200; DB 3; Length 357;
Best Local Similarity 63.9%; Pred. No. 5.3e-19;
Matches 39; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY      4 WGEFQVDGRSARGGCQTSNDAAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSNLDRI 63
Db      111 FGVSIQIDGRSARGGQSQSANDAYAEALNSGSKSEALNLIKKEAPKDYILQFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

RESULT 15
US-08-838-151A-27
; Sequence 27, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS: 63
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-27
```

```
Query Match      55.4%; Score 200; DB 3; Length 357;
Best Local Similarity 63.9%; Pred. No. 5.3e-19;
Matches 39; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY      4 WGEFQVDGRSARGGCQTSNDAAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSNLDRI 63
Db      111 FGVSIQIDGRSARGGQSQSANDAYAEALNSGSKSEALNLIKKEAPKDYILQFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171
```

Search completed: December 23, 2003, 08:59:33
Job time : 11.6667 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	361	100.0	70	10	US-09-289-346A-4	Sequence 4	
2	346	95.8	70	10	US-09-289-346A-1	Sequence 1	
3	346	95.8	356	10	US-09-289-346A-11	Sequence 11	
4	338	93.6	70	10	US-09-289-346A-9	Sequence 9	
5	335	92.8	70	10	US-09-289-346A-12	Sequence 12	
6	334	92.5	70	10	US-09-289-346A-16	Sequence 16	
7	332	92.0	70	10	US-09-289-346A-8	Sequence 8	
8	332	92.0	70	10	US-09-289-346A-14	Sequence 14	
9	331	91.7	70	10	US-09-289-346A-2	Sequence 2	
10	331	91.7	70	10	US-09-289-346A-10	Sequence 10	
11	330	91.4	70	10	US-09-289-346A-13	Sequence 13	
12	328	90.9	70	10	US-09-289-346A-15	Sequence 15	
13	325	90.0	70	10	US-09-289-346A-5	Sequence 5	
14	324	89.8	70	10	US-09-289-346A-7	Sequence 7	
15	322	89.2	70	10	US-09-289-346A-6	Sequence 6	

```

Query Match      100.0%; Score 361; DB 10; Length 70;
Best Local Similarity 100.0%; Pred. No. 1e-40;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCQTSNDAAAEALNWSKKEALQITAAAIPEKYLEQFHNLSNL 60
Db 1 TLVWGEFQVDRSARGCQTSNDAAAEALNWSKKEALQITAAAIPEKYLEQFHNLSNL 60
QY 61 DRIFDKTPEP 70

```

```

Db          61 DRIFDKTPEP 70
|||||
110 TLVWGEFQVDRSARGGCQTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 169

RESULT 2
US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1

Query Match          95.8%; Score 346; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 1e-38; 3; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSDNDAAEALNASSKEALQIIAAIPEKYLFOFHNLSNL 60
Db 1 TLVWGEFQVDRSARGGCQTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
|||||
61 DRIFDKTPEP 70

RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match          95.8%; Score 346; DB 10; Length 356;
Best Local Similarity 95.7%; Pred. No. 8.9e-38; 3; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSDNDAAEALNASSKEALQIIAAIPEKYLFOFHNLSNL 60
|||||
110 TLVWGEFQVDRSARGGCQTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 169

Db          61 DRIFDKTPEP 70
|||||
170 DRIFDKTPEP 179

RESULT 4
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match          93.6%; Score 338; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 1.2e-37; 4; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSDNDAAEALNASSKEALQIIAAIPEKYLFOFHNLSNL 60
Db 1 TLVWGEFQVDRSARGGCQTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
|||||
61 DRIFDKTPEP 70

RESULT 5
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12

Query Match          92.8%; Score 335; DB 10; Length 70;

```



```

; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
; US-09-289-346A-2

Query Match          91.7%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1e-36;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIIAAIPKYLQFHNLSNL 60
DB 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIIREKIPKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LLLL136).
; US-09-289-346A-10

Query Match          91.7%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1e-36;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIIAAIPKYLQFHNLSNL 60
DB 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIIREKIPKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LLLL136).
; US-09-289-346A-13

Query Match          91.7%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1e-36;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIIAAIPKYLQFHNLSNL 60
DB 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIIREKIPKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 15
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LLLL136).
; US-09-289-346A-15

Query Match          90.9%; Score 328; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 2.6e-36;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIIAAIPKYLQFHNLSNL 60
DB 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIIREKIPKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS

```

```

; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (EKY159->AAA159).
US-09-289-346A-5

Query Match      90.0%; Score 325; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 6.7e-36;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIAAAIPEKYL FQFHNLSNL 60
Db 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPAAAL FQFHNLSNL 60

QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 14
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDRI172->ALAA172).
US-09-289-346A-7

Query Match      89.8%; Score 324; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 9.1e-36;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIAAAIPEKYL FQFHNLSNL 60
Db 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYL FQFHNLSAL 60

QY 61 DRIFDKTPEP 70
Db 61 AAIFDKTPEP 70
```

```

RESULT 15
US-09-289-346A-6
; Sequence 6, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (52)..(55)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (QFHN165->AFAA165).
US-09-289-346A-6

Query Match      89.2%; Score 322; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.7e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIAAAIPEKYL FQFHNLSNL 60
Db 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYL FQFHNLSNL 60

QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

Search completed: December 23, 2003, 09:43:29
Job time : 76 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds
(without alignments)
673.181 Million cell updates/sec

Title: US-09-289-346B-4
Perfect score: 361
Sequence: 1 TLVWGEFQVDSARGGCGT.....PQFHNLSNLDRIFDKTPPEP 70

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	346	95.8	352	1 QOCVLI	AL1 protein - toma
2	249	69.0	361	1 QOCVPT	AL1 protein - pota
3	240	66.5	358	2 S07594	hypothetical prote
4	233	64.5	362	1 JQ1887	AL1 protein - toma
5	229	63.4	359	2 S39211	gene C1 protein -
6	222	61.5	349	2 JQ2300	replicase - pepper
7	222	61.5	349	2 S31875	AL1 protein - pepp
8	222	61.5	359	2 S22593	hypothetical prote
9	219	60.7	359	2 S39235	gene C1 protein -
10	216	59.8	351	2 JQ2327	AL1 protein - Indi
11	216	59.8	355	1 QOCVM1	AV1 protein - abut
12	213	59.0	385	2 S28360	AL1 protein - beet
13	210	58.2	358	1 JQ1870	AL1 protein - toma
14	200	55.4	357	1 QOCVC1	AL1 protein - toma
15	199	55.1	360	2 S59885	replication-associ
16	134	37.1	131	2 S45059	AC1 protein (clone
17	128	35.5	347	1 QOCVS1	AL1 protein - squa
18	72	19.9	587	2 JG1419	Fc gamma (IgG) rec
19	68	18.8	714	2 C95382	probable ferrichro
20	63.5	17.6	584	2 T19061	hypothetical prote
21	62.5	17.3	1006	2 S74992	hypothetical prote
22	61.5	17.0	299	2 B71967	probable peptidyl-
23	61.5	17.0	335	1 DBBSGF	glyceroldehyde-3-p
24	61.5	17.0	481	2 A70091	probable phosphos
25	61.5	17.0	1044	2 A70091	protein kinase sub
26	61.5	17.0	1203	2 T17415	mycelial surface a
27	61.5	17.0	1229	2 T48959	kinesin-like prote
28	60.5	16.8	159	2 C71838	NADH2 dehydrogenas
29	60.5	16.8	159	2 E64677	NADH2 dehydrogenas

30	60.5	16.8	819	2	AI3197	TonB-dependent rec
31	60	16.6	767	2	F71479	hypothetical prote
32	60	16.6	1008	2	T41244	SEC14 protein homo
33	59	16.3	160	2	G82060	hypothetical prote
34	59	16.3	201	2	AE2732	NADH ubiquinone ox
35	59	16.3	201	2	G97513	NADH dehydrogenase
36	59	16.3	228	2	F90130	hypothetical prote
37	59	16.3	338	2	AG3582	iron(III)-binding
38	59	16.3	1502	1	RGBYH1	CYC1/CYP3 transcr1
39	58.5	16.2	297	1	MNVNRV	nonstructural prot
40	58.5	16.2	357	2	T02246	protein C17D12-7 (
41	58.5	16.2	569	2	H87926	hypothetical prote
42	58.5	16.2	642	2	D90558	topoisomerase iv s
43	58.5	16.2	769	2	F81742	conserved hypothet
44	58.5	16.2	2135	2	T14602	variant-specific s
45	58	16.1	345	2	AD3024	hypothetical prote

ALIGNMENTS

RESULT 1

QOCVLI
AL1 protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994
C:Accession: A04170
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
A:Residues: 1-352 <HAM>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match	95.8%	Score	346;	DB	1;	Length	352;
Best Local Similarity	95.7%	Pred. No.	4.2e-33;	Mismatches	3;	Indels	0;
Matches	67;	Conservative	0;	0;	Gaps	0;	
QY	1	TLVWGEFQVDSARGGCGTGNDAAAEALNASSKEEALQIIAAAIPEKYLFOFHNLSNL	60				
DB	111	TLVWGEFQVDSARGGCGTGNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL	170				
QY	61	DRIFDKTPPEP	70				
DB	171	DRIFDKTPPEP	180				

RESULT 2

QOCVPT
AL1 protein - potato yellow mosaic virus (isolate Venezuela)
C:Species: potato yellow mosaic virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C:Accession: J00364
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel
A:Reference number: J00362; MUID:91311403; PMID:1856690
A:Accession: J00364
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-361 <COU>
A:Cross-references: GB:D00940; NID:g222458; PIDN:BAA00782.1; PID:g222459
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 69.0%; Score 249; DB 1; Length 361;
Best Local Similarity 68.1%; Pred. No. 1.3e-21;
Matches 47; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGCGCQTSNDAAAEALNASSKEALQIIAAAIPEKYLFOFHNLSNL 60
DB 110 TLVWGFQVDSARGCGCQTSNDAAAEALNASSKEALQIIAAAIPEKYLFOFHNLSNL 169
QY 61 DRIFDKTPE 69
DB 170 DRIFDKAPE 178

RESULT 3

S07594
hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)
C/Species: cassava latent virus
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C/Accession: S07594
R/Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
Nucleic Acids Res. 18, 197-198, 1990
A/Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A/Reference number: S07590; MUID:90174930; PMID:2308831
A/Accession: S07594
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-358 <MOR>
A/Cross-references: EMBL:X17095; NID:G59371; PIDN:CAA34953.1; PID:G59376
C/Genetics:
A/Map position: segment DNAL
C/Superfamily: tomato golden mosaic virus ALL protein

Query Match 66.5%; Score 240; DB 2; Length 358;
Best Local Similarity 61.4%; Pred. No. 1.5e-20;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGCGCQTSNDAAAEALNASSKEALQIIAAAIPEKYLFOFHNLSNL 60
DB 109 TLVWGFQVDSARGCGCQTSNDAAAEALNASSKEALQIIAAAIPEKYLFOFHNLSNL 168
QY 61 DRIFDKTPE 70
DB 169 DRIFQEPAP 178

RESULT 4

JQ1887
ALL protein - tomato yellow leaf curl virus (strain Australia)
N/Alternate names: CI protein
C/Species: tomato yellow leaf curl virus
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
C/Accession: JQ1887
R/Dry, I.B.; Rigden, J.E.; Krake, L.R.; Mullineaux, P.M.; Rezaian, M.A.
J. Gen. Virol. 74, 147-151, 1993
A/Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.
A/Reference number: JQ1885; MUID:93139778; PMID:8423446
A/Accession: JQ1887
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-362 <DRY>
A/Cross-references: GB:S53251
C/Superfamily: tomato golden mosaic virus ALL protein

Query Match 64.5%; Score 233; DB 1; Length 362;
Best Local Similarity 54.1%; Pred. No. 1e-19;
Matches 46; Conservative 9; Mismatches 14; Indels 16; Gaps 1;

QY 1 TLVWGFQVDSARGCGCQTSNDAAAEALNASSKEALQIIAAAIPEKYLFOFHNLSNL 60
DB 110 TLVWGFQVDSARGCGCQTSNDAAAEALNASSKEALQIIAAAIPEKYLFOFHNLSNL 169
QY 61 DRI-----FDKTP 69
|||

DB 170 DRIFPPLEVYVSPFLSSSFDVRPE 194

RESULT 5

S39211
gene CI protein - tomato yellow leaf curl virus
C/Species: tomato yellow leaf curl virus
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C/Accession: S39211
R/Noris, E.; Hidalgo, E.; Accotto, G.; Morionese, B.
submitted to the EMBL Data Library, August 1993
A/Description: High similarity among the tomato yellow leaf curl virus isolates from th
A/Reference number: S39209
A/Accession: S39211
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-359 <NOR>
A/Cross-references: EMBL:Z25751; NID:G433655; PIDN:CAA81026.1; PID:G433658
C/Superfamily: tomato golden mosaic virus ALL protein

Query Match 63.4%; Score 229; DB 2; Length 359;
Best Local Similarity 60.9%; Pred. No. 3e-19;
Matches 42; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGFQVDSARGCGCQTSNDAAAEALNASSKEALQIIAAAIPEKYLFOFHNLSNL 61
DB 111 LVWGFQVDSARGCGCQTSNDAAAEALNASSKEALQIIAAAIPEKYLFOFHNLSNL 170
QY 62 RIFDKTPE 70
DB 171 RVFQVPPAP 179

RESULT 6

JQ2300
replicase - pepper huasteco virus (component A)
N/Alternate names: ORF ALL protein
C/Species: pepper huasteco virus
C/Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Sep-1999
C/Accession: JQ2300
R/Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estrella, L.; Rivera-Bustamante, R.
J. Gen. Virol. 74, 2225-2231, 1993
A/Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with b1
A/Reference number: JQ2299; MUID:94015007; PMID:8409944
A/Accession: JQ2300
A/Molecule type: DNA
A/Residues: 1-349 <TOR>
A/Cross-references: GB:X70418; NID:G61023; PIDN:CAA49856.1; PID:G61025
C/Superfamily: tomato golden mosaic virus ALL protein

Query Match 61.5%; Score 222; DB 2; Length 349;
Best Local Similarity 60.0%; Pred. No. 1.9e-18;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGCGCQTSNDAAAEALNASSKEALQIIAAAIPEKYLFOFHNLSNL 60
DB 110 TLVWGFQVDSARGCGCQTSNDAAAEALNASSKEALQIIAAAIPEKYLFOFHNLSNL 169
QY 61 DRIFDKTPE 70
DB 170 NRIFQTPPEP 179

RESULT 7

S31875
ALL protein - pepper rizado amarillo virus
C/Species: pepper rizado amarillo virus
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 20-Sep-1999
C/Accession: S31875
R/Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-I
submitted to the EMBL Data Library, February 1993
A/Description: Complete nucleotide sequence of pepper huasteco virus: analysis and com
A/Reference number: S31872

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds
(without alignments)
569.747 Million cell updates/sec

Title: US-09-289-346B-4

Perfect score: 361

Sequence: 1 TLVWGEFQVDRSARGGCQT.....PQHNLNSLDRFDKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	95.8	352	1 VAL1 TGMV	P03567 tomato gold
2	249	69.0	361	1 VAL1 PYMVV	P27258 potato yell
3	240	66.5	358	1 VAL1 CLVK	P14982 cassava lat
4	240	66.5	358	1 VAL1 CLVN	P14972 cassava lat
5	233	64.5	362	1 VAL1 TYLCA	P36279 tomato yell
6	229	63.4	359	1 VAL1 TYLCU	P38609 tomato yell
7	222	61.5	349	1 VAL1 PHUV	P06923 pepper huas
8	222	61.5	359	1 VAL1 TYLCM	P27260 tomato yell
9	217	60.1	353	1 VAL1 BGMV	P05175 bean golden
10	216	59.8	355	1 VAL1 ABMVW	P21947 abutilon mo
11	213	59.0	358	1 VAL1 ECTV	P14991 beet curly
12	210	58.2	361	1 VAL1 TMOV	P06657 tomato mott
13	200	55.4	357	1 VAL1 TYLCV	P27259 tomato yell
14	128	35.5	347	1 VAL1 SLVC	P29048 squash leaf
15	61.5	17.0	299	1 Y175 HELRU	Q92mg7 helicobacte
16	61.5	17.0	334	1 G3P_BACST	P00362 bacillus st
17	61.5	17.0	335	1 G3P_BACCO	P15115 bacillus co
18	61.5	17.0	1044	1 BUB1 SCHPO	Q94751 schizosacch
19	60	16.6	1008	1 YX4 SCHPO	Q9uu99 schizosacch
20	59	16.3	1502	1 CYP1 YEAST	P12351 saccharomyc
21	58.5	16.2	297	1 RRPB_RABVP	P06747 rabies viru
22	58	16.1	492	1 MOT3 MOUSE	P03308 mus musculu
23	58	16.1	492	1 MOT3 RAT	O70461 rattus norv
24	58	16.1	555	1 GLPD_BACSU	P18158 bacillus su
25	58	16.1	601	1 CYSJ_BUCAI	P57503 buchnera ap
26	57.5	15.9	396	1 DXR_XANAC	O8pm11 xanthomonas
27	57	15.8	223	1 DGK2 LACAC	O59484 lactobacill
28	57	15.8	316	1 SPDE_COPAR	O82147 coffea arab
29	57	15.8	379	1 CYB_ASTPE	Q33818 asterina pe
30	57	15.8	387	1 Y4PF_RHISN	P55615 rhizobium s
31	57	15.8	836	1 GCSR_HUMAN	Q99062 homo sapien
32	57	15.8	1287	1 SKI2 YEAST	P35207 saccharomyc
33	56.5	15.7	863	1 AMPN_CAUCR	P37893 caulobacter

34 56 15.5 367 1 LHX4 MOUSE P53776 mus musculu
35 56 15.5 476 1 DGR8 HUMAN Q96df8 homo sapien
36 56 15.5 479 1 DGR8 MOUSE O70279 mus musculu
37 56 15.5 577 1 PTLB_LACCA P24400 lactobacill
38 56 15.5 874 1 SLAP_BACLI P49052 bacillus li
39 55.5 15.4 298 1 OLG2_CHICK Q90xb3 gallus gall
40 55.5 15.4 299 1 Y175_HELPY P56112 helicobacte
41 55.5 15.4 323 1 VAL1_PASVK Q00338 panicum str
42 55.5 15.4 397 1 METL_RAT P13444 rattus norv
43 55.5 15.4 428 1 GBA1_CANAL P28868 candida alb
44 55.5 15.4 468 1 AMPA_NEIMA Q91ti8 neisseria m
45 55.5 15.4 515 1 LEU1_BACHD Q98e8 bacillus ha

ALIGNMENTS

RESULT 1
VAL1 TGMV STANDARD; PRT; 352 AA.
AC P03567;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Tomato golden mosaic virus (TGMV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10831;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;
RT "Complete nucleotide sequence of the infectious cloned DNA components of tomato golden mosaic virus: potential coding regions and regulatory sequences."
RL EMBO J. 3:2197-2205(1984).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

EMBL; K02029; -; NOT_ANNOTATED_CDS.
DR PIR; A04170; Q0CVL1; Gemini_All.
DR InterPro; IPR001191; Gemini_All.
DR Pfam; PF00799; Gemini_All; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_All; 1.
KW ATP-binding.
FT NP BIND 223 230 ATP (POTENTIAL).
SQ SEQUENCE 352 AA; 40332 MW; C33C938S9644B44 CRC64;

Query Match 95.8%; Score 346; DB 1; Length 352;
Best Local Similarity 95.7%; Pred. No. 2.3e-34;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEEALQITAAAIPEKYLQFHNLSNL 60
DB 111 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEEALQITREIKPEKYLQFHNLSNL 170
QY 61 DRIFDKTPPEP 70
DB 171 DRIFDKTPPEP 180

RESULT 2
VAL1 PYMVV STANDARD; PRT; 361 AA.
ID VAL1 PYMVV
AC P27258;

```

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus.";
RL J. Gen. Virol. 72:1515-1520(1991).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D00940; BAA00782.1; -.
DR PIR; J00364; Q0CVPT.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding. 222 229 ATP (POTENTIAL).
KW NP BIND 361 AA; 40850 MW; 5627A33BF1264383 CRC64;
FT SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;
SQ -----
Query Match
Best Local Similarity 69.0%; Score 249; DB 1; Length 361;
Matches 47; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGRGCGQTSNDAAALNASKEALQIIAAAIPEKYLQFPHNLSNL 60
Db 110 TIEWGLFQIDGRSGRGCGQTSNDAAALNASKEALQIIAAAIPEKYLQFPHNLSNL 169
QY 61 DRIFDKTPE 69
Db 170 DRIFDKAPE 178

RESULT 3
VAL1_CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

```

CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753BE92D69 CRC64;

Query Match
Best Local Similarity 66.5%; Score 240; DB 1; Length 358;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGRGCGQTSNDAAALNASKEALQIIAAAIPEKYLQFPHNLSNL 60
Db 109 TVEWGQFQIDGRSGRGCGQTSNDAAALNASKEALQIIAAAIPEKYLQFPHNLSNL 168
QY 61 DRIFDKTPE 70
Db 169 DRIFQEPAP 178

RESULT 4
VAL1_CLVN STANDARD; PRT; 358 AA.
ID AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
RL Nucleic Acids Res. 18:197-198(1990).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X17095; CAA34953.1; -.
DR PIR; S07594; S07594.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16B80CB2D5E2C CRC64;

Query Match
Best Local Similarity 66.5%; Score 240; DB 1; Length 358;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGRGCGQTSNDAAALNASKEALQIIAAAIPEKYLQFPHNLSNL 60
Db 109 TVEWGQFQIDGRSGRGCGQTSNDAAALNASKEALQIIAAAIPEKYLQFPHNLSNL 168
QY 61 DRIFDKTPE 70
Db 169 DRIFQEPAP 178

```



```

QY 61 DRIFDKTPEP 70
DB 170 NRIFQTPPEP 179

RESULT 8
ID VAL1 TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92107660; PubMed=1840676;
RA Kheyr-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a
RT whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X61153; CAA43466.1; -
DR PIR; S22593; S22593.
DR PDB; 1L2M; 18-SEP-02.
DR PDB; 1L5I; 18-SEP-02.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding; 3D-structure.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 40733 MW; 9717B4A07C93EFA7 CRC64;

Query Match 61.5%; Score 222; DB 1; Length 359;
Best Local Similarity 58.0%; Pred. No. 2.5e-19;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRSGSGCQTSDAAAEALNASSKEEALQIAAAIPEKYLQFHNLSNLD 61
DB 111 LEWGTQFIDGSRAGGQQTANDAYAKAINAGSKSQALDVIKELAPRDVILHFNHNSNLD 170

QY 62 RIFDKTPEP 70
DB 171 KVQVPPAP 179

RESULT 9
ID VAL1 BGWV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE AL1 protein (40.2 kDa protein).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
RT regulation in geminiviruses";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M10070; AAA46318.1; -
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 60.1%; Score 217; DB 1; Length 353;
Best Local Similarity 60.0%; Pred. No. 1e-18;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLWGEFQVDRSGSGCQTSDAAAEALNASSKEEALQIAAAIPEKYLQFHNLSNLD 60
DB 110 TIENGQFQVDRSGSGCQTSDAAAEALNASSKEEALQIAAAIPEKYLQFHNLSNLD 169

QY 61 DRIFDKTPEP 70
DB 170 ERIFKTPPEP 179

RESULT 10
ID VAL1 ABMV STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimmat G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X15983; -; NOT_ANNOTATED_CDS.
DR PIR; A36214; QQCVM1.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.

```

```

FT NP BIND 221 228 ATP (POTENTIAL)
SQ SEQUENCE 355 AA; 40257 MW; 16A2CABA63251E95 CRC64;

Query Match
Best Local Similarity 59.8%; Score 216; DB 1; Length 355;
Matches 41; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSRGSGCQTSDNDAEALNASKEEALQIIAAIPEKYLFOFHNLSNL 60
DB 110 TAEWGFQVDSRGSGCQTSDNDAEALNASKEEALQIIAAIPEKYLFOFHNLSNL 169

QY 61 DRIFDKTPPEP 70
DB 170 ERIFAKAPEP 179

RESULT 11
ID VAL1_BCTV STANDARD; PRT; 358 AA.
AC P14991;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
CX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
RT beet curly top virus."
RL EMBO J. 5:1761-1767(1986).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X04144; -; NOT ANNOTATED CDS.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match
Best Local Similarity 59.0%; Score 213; DB 1; Length 358;
Matches 39; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSRGSGCQTSDNDAEALNASKEEALQIIAAIPEKYLFOFHNLSNL 60
DB 110 TIEWGFQVDSRGSGCQTSDNDAEALNASKEEALQIIAAIPEKYLFOFHNLSNL 169

QY 61 DRIFDKTPPEP 70
DB 170 QKIFQPPDP 179

RESULT 12
ID VAL1_TMOV STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.

```

```

GN AL1.
OS Tomato mottle virus (isolate Florida) (TMOV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
CX NCBI_TaxID=36449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93107858; PubMed=1469361;
RA Abouzid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida."
RL J. Gen. Virol. 73:3225-3229(1992).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L14460; AAC32414.1; -
CC PIR; JQ1870; JQ1870.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
FT NP BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 813B865CEBAC6950 CRC64;

Query Match
Best Local Similarity 58.2%; Score 210; DB 1; Length 361;
Matches 38; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSRGSGCQTSDNDAEALNASKEEALQIIAAIPEKYLFOFHNLSNL 60
DB 110 TIEWGFQVDSRGSGCQTSDNDAEALNASKEEALQIIAAIPEKYLFOFHNLSNL 169

QY 61 DRIFDKTPPEP 70
DB 170 ERIFAKAPEP 179

RESULT 13
ID VAL1_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
CX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92024070; PubMed=1926771;
RA Navot N., Pichersky E., Zeldan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component."
RL Virology 185:151-161(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----

```

```
DR EMBL; X15656; CAA33688.1; -.
DR PIR; D40779; QOCVC1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALI.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 219 226 ATP (POTENTIAL).
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match 55.4%; Score 200; DB 1; Length 357;
Best Local Similarity 63.9%; Pred. No. 1.2e-16;
Matches 39; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 4 WGEFQVDRSGRGCCGTSNDAAAEALNASSKEALQIIAAAIPEKYLQFPHNLNSLDR 63
Db 111 FGVSDIGRSARGCQGSANDAYAEALNASSKEALNIIKAKPKDYILOFHNLSNLDRI 170

QY 64 F 64
Db 171 F 171

RESULT 14
VAL1 SLCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G., Laxdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic components of a bipartite squash leaf curl geminivirus with a broad host range phenotype."
RL Virology 180:58-69(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
CC EMBL; M38183; AAC32410.1; ALT_INIT.
DR PIR; G36785; QOCVS1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALI.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDAEBDD122110E CRC64;

Query Match 35.5%; Score 128; DB 1; Length 347;
Best Local Similarity 39.4%; Pred. No. 6e-08;
Matches 26; Conservative 13; Mismatches 23; Indels 4; Gaps 1;

QY 5 GEFQVDRSGRGCCGTSNDAAAEALNASSKEALQIIAAAIPEKYLQFPHNLNSLDR 64
Db 116 GQYKVSQ-----GSKNKDDVYHNNAVAGSAGEALDIKAGDPKTFIVYHNLLANVERLF 171

QY 65 DKTPPEP 70
Db 172 QKPEP 177
```

RESULT 15

```
Y175 HELPJ STANDARD; PRT; 299 AA.
ID Y175_HELJP
AC Q9ZMQ7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein JHP0161 precursor.
GN JHP0161.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.;
RA "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori."
RT Nature 397:176-180(1999).
RL Nature 397:176-180(1999).
CC -!- SIMILARITY: BELONGS TO THE PPIC/PARVULIN FAMILY OF ROTAMASES.
CC
CC STRONG, TO C.JEJUNI CBF2.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
CC EMBL; AB001454; AA005744.1; -.
DR PIR; B71967; B71967.
DR HSSP; Q9Y237; 1RQ3.
DR InterPro; IPR000297; Rotamase.
DR Pfam; PF00639; Rotamase; 1.
DR PROSITE; PS01096; PPIC_PPIASE_1; 1.
DR PROSITE; PS01096; PPIC_PPIASE_2; 1.
DR KW Hypothetical protein; Isomerase; Rotamase; Signal; Complete proteome.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 299 HYPOTHETICAL PROTEIN JHP0161.
FT DOMAIN 154 253 PPIC.
SQ SEQUENCE 299 AA; 34040 MW; 9C037B1CD1110143 CRC64;

Query Match 17.0%; Score 61.5; DB 1; Length 299;
Best Local Similarity 28.1%; Pred. No. 5.8;
Matches 18; Conservative 12; Mismatches 13; Indels 21; Gaps 2;

QY 22 NDAAAEALNASSKEALQIIAAAIPEKYLQFPHNLNSLDR 62
Db 93 NEAKAEKLNQTPPEFKAMMEAVKQALVEFWAKQAEVKKIQIPEKMQDFY--NANKDQ 150

QY 63 IFDK 66
Db 151 LFKV 154

Search completed: December 23, 2003, 08:57:38
Job time : 6.77778 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 25.3333 Seconds
(without alignments)
713.040 Million cell updates/sec

Title: US-09-289-346B-4
 Perfect score: 361
 Sequence: 1 TLWGEFQVDSARGGQT.....FQHNLSNLDRIFDKTPP 70

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

```
Minimum DB seq length: 0
Maximum DB seq length: 200000000
```

Post-processing: Minimum Match 0%

Topic Processing: Minimum Match 0%
Maximum Match 100%

Maximum match 100%
Listing first 45 summaries

Database :

```

1: sp archaea.*
2: sp bacteria.*
3: sp fungi.*
4: sp human.*
5: sp invertebrate.*
6: sp mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_vertebrat.*
17: sp_archaeap.*

```

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	297	82.3	351	12	Q91R10	Q91R10	tomato seve
2	295	81.7	352	12	Q9E000	Q9E000	tomato rugo
3	290	80.3	322	12	Q8QV3	Q8QV3	tomato chlo
4	281	77.8	236	12	Q9WHF6	Q9WHF6	tomato mild
5	281	77.8	226	12	O09727	O09727	leonurus mo
6	277	77.3	361	12	Q67574	Q67574	bean golden
7	277	76.7	225	12	Q9QDB1	Q9QDB1	cowpea gold
8	274	75.9	314	12	Q9ELT8	Q9ELT8	sweet potat
9	274	75.9	364	12	Q9Q555	Q9Q555	sweet potat
10	271	75.1	185	12	Q8E693	Q8E693	sida golden
11	270	74.8	235	12	Q8QP4	Q8QP4	tomato infe
12	269	74.5	208	12	Q8JLY3	Q8JLY3	potato yell
13	269	74.5	289	12	Q8JUY5	Q8JUY5	potato yell
14	266	73.7	149	12	P88975	P88975	macroptiliu
15	266	73.7	333	12	Q9YLA4	Q9YLA4	macroptiliu
16	265	73.4	361	12	Q8JmJ4	Q8JmJ4	potato yell

17	261	72.3	361	12	Q8QVH0	Q8qvh0	ageratum en
18	260	72.0	334	12	Q8QVH0	Q8qvh0	ageratum en
19	260	72.0	360	12	Q8QVH0	Q8qvh0	ageratum en
20	255	70.6	223	12	Q8QPU7	Q8qpU7	sida mottle
21	254	70.4	190	12	Q8Q089	Q8z089	tomato seve
22	254	70.4	190	12	Q8Q084	Q8z084	tobacco lea
23	253	70.1	190	12	Q8Q827	Q8w827	tobacco lea
24	253	70.1	208	12	Q8Z0C4	Q8z0C4	tobacco lea
25	253	70.1	359	12	Q8J1M8	Q8j1m8	tobacco lea
26	253	70.1	359	12	Q8JVE8	Q8jve8	tomato curl
27	251	69.5	208	12	Q8Z0C0	Q8z0C0	tobacco lea
28	251	69.5	208	12	Q8Z0B8	Q8z0B8	tobacco lea
29	251	69.5	363	12	Q8Z719	Q8z719	cotton leaf
30	251	69.5	363	12	Q8Z705	Q8z705	cotton leaf
31	249	69.0	208	12	Q8Z0B6	Q8z0B6	tobacco lea
32	248	68.7	203	12	Q8Z083	Q8z083	tobacco lea
33	248	68.7	359	12	Q8YZV4	Q8yzv4	tomato yell
34	248	68.7	359	12	Q8YUX7	Q8yux7	tomato yell
35	248	68.7	359	12	Q8YL27	Q8yl27	tomato yell
36	248	68.7	359	12	Q8YZV2	Q8yzv2	tomato yell
37	248	68.7	363	12	Q8Z357	Q8z357	cotton leaf
38	247	68.4	359	12	Q8JNG3	Q8jng3	cotton leaf
39	247	68.4	359	12	Q88942	Q88942	tomato yell
40	245	67.9	307	12	Q81ET7	Q8iet7	cotton leaf
41	245	67.9	361	12	Q8Z723	Q8z723	cotton leaf
42	245	67.9	363	12	Q8JLK6	Q8jlk6	cotton leaf
43	244	67.6	348	12	Q81LW5	Q8llw5	macroptiliu
44	243	67.3	359	12	Q81B86	Q81b86	ageratum ye
45	243	67.3	360	12	Q8PD10	Q8pd10	ageratum ye

ALIGNMENTS

RESULT 1

Q9IR10	PRELIMINARY;	PRT;	351 AA.
ID	Q9IR10		
AC	Q9IR10;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Rep protein.		
DE	ACL.		
GN	Tomato severe rugose virus.		
OS	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.		
OC	NCBI_TaxID=158463;		
OX	[1]		
RN	SEQUENCE FROM N.A.		
RP	STRAIN=Minas Gerais;		
RC	Rezendez W.L., Goulart L.R., Parreira K.S., Figueiredo		
RC	The full-length DNA-A nucleotide sequence of a novel		
RT	Begomovirus, Tomato severe rugose virus, in Brazil.		
RT	Submitted (APR-2001) to the EMBL/GenBank/DBJ database.		
RL	EMBL; AY029750; AA050357.1; --		
DR	InterPro: IPR001191; Gemini AL1.		
DR	Pfam: PF00799; Gemini AL1; 1.		
DR	PRINTS: PR00227; GEMCOATL1.		
DR	ProDom: PD000736; Gemini AL1; 1.		
DR	SEQUENCE 351 AA; 40122 MW; 87E937A4F873B6CF C		

Query Match 82.3%; Score 297; DB 12; Length 351;
Best Local Similarity 78.6%; Pred. No. 1.7e-27;
Matches 55; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy	1	TLTWGEFQVDGSRAGCGCOTSDNDAAEAALNAAKKEALQIIAAAIPEKYLQFQHNLSNL	60
		: : : : : : :	
Db	111	TLTWEGFQDGRSARGCGCOTANDAAEAALNAPSQVVALQIIREKLPEKFLQFQHNLSNL	170
		: : : : : :	
Qy	61	DRIFDKTPEP	70
		: :	
Db	171	DRIFARAPEP	180
		: :	

DT	01-MAY-2000	(TReMBLrel. 13, Created)
DT	01-MAY-2000	(TReMBLrel. 13, Last sequence update)
DT	01-JUN-2002	(TReMBLrel. 21, Last annotation update)
DE	REPLICATION ASSOCIATED PROTEIN (Fragment).	
GN	RSP.	
OS	Cowpea golden mosaic virus.	
OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.	
NCBI_TaxID=69263;	[1]	
RN	SEQUENCE FROM N.A.	
RC	STRAIN=CGMV-BR;	
RA	Faria J.C.;	
RT	"Partial nucleotide sequence of cowpea golden mosaic geminivirus from Brazil."	
RL	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL; AF18708; AAF06318.1; -	
DR	InterPro; IPR001191; Gemini_AL1.	
DR	Pfam; PF00799; Gemini_AL1; I.	
DR	PRINTS; PR00227; GEMCOATALL1	
DR	ProDom; PD000736; Gemini_AL1; 1.	
FT	NON_TER 225	
SQ	SEQUENCE 225 AA; 25766 MW; 1089CBBD8D15B5D CRC64;	
	Query Match 76.7%; Score 277; DB 12; Length 225;	
	Best Local Similarity 77.6%; Pred.No. 2.6e-25;	
	Matches 52; Conservative 7; Mismatches 8; Indels 0; Gaps 0;	
Qy	4 WGFQVDFGRSGGCGCTSNDAAEALNASKKERALQITAAAIPEKYLFOFHNLNSLDRI 63 : : : : : : : : : : :	
Dd	113 WGHFQIDGRSGGGQQQTINDAAGEALNASKKERAMQIKKEKLPEKFYQVHNLSNLDRI 172 : : : : : : : : : :	
Qy	64 FDKTPRP 70	
Dd	173 FKAPPEP 179	
RESULT 8		
Q9ELT8	PRELIMINARY;	PRT; 314 AA.
ID	OSELT8	
AC	QSELT8	
DT	01-MAR-2001	(TReMBLrel. 16, Created)
DT	01-MAR-2001	(TReMBLrel. 16, Last sequence update)
DT	01-DEC-2001	(TReMBLrel. 19, Last annotation update)
DE	Replication association protein.	
GN	Acl.	
OS	Sweet potato leaf curl virus.	
OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.	
NCBI_TaxID=100755;	[1]	
RN	SEQUENCE FROM N.A.	
RP	Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;	
RT	"Detection of a geminivirus infecting sweet potato in the United States.";	
RL	Plant Dis. 82:1253-1257(1998).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RA	Lotrakul P., Valverde R.A.;	
DL	Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.	
RL	EMBL; AF288227; AGO1006.1; -	
DR	InterPro; IPR001191; Gemini_AL1.	
DR	Pfam; PF00799; Gemini_AL1; I.	
DR	PRINTS; PR00227; GEMCOATALL1	
DR	ProDom; PD000736; Gemini_AL1; 1.	
SQ	SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;	
	Query Match 75.9%; Score 274; DB 12; Length 314;	
	Best Local Similarity 79.4%; Pred.No. 9.1e-25;	
	Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;	
Qy	1 TLVWGEFQVDGRSGGCCTSNDAEAALNASKKERALQITAAAIPEKYLFOFHNLNSLN 60 : : : : : : : : : : :	
Dd	110 TTWGFEQVDGRSGGCQTANDAAEALNAGSKREALQIIRKLEPKYLFOFHNLVSNN 169 : : : : : : : : : :	

```

QY 61 DRIPDKTP 68
Db 170 DRIFSPPP 177

RESULT 9
Q98555 PRELIMINARY; PRT; 364 AA.
AC Q98555;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De la Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RN Plant Dis. 82:1253-1257(1998).
[2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RN Virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0(1999).
DR EMBL: AF104036; AAD47173.1; -.
DR InterPro: IPR001191; Geminini AL1.
DR Pfam: PF00799; Geminini AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Geminini AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 75.98; Score 274; DB 12; Length 364;
Best Local Similarity 79.48; Pred. No. 1.1e-24;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSARGCGCOTSDAAAEALNASSKEEALQIIAAAIPEKYLQFPHNLNSL 60
Db 110 TITWGFQVDRSARGCGCQTANDAAAEALNASSKEEALQIIREKLPKYLQFPHNLVSNL 169

QY 61 DRIPDKTP 68
Db 170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica;
RA Roye M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed
RN species Sida spp, Macroptilium lathyroides, and Wissadula amplissima
RL from Jamaica.";
RL Plant Dis. 81:1251-1258(1997).
DR EMBL: U67926; AAB97865.1; -.
DR InterPro: IPR001191; Geminini AL1.
DR Pfam: PF00799; Geminini AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.

QY 61 DRIPDKTP 68
Db 170 DRIFSPPP 177

RESULT 11
Q8QP04 PRELIMINARY; PRT; 235 AA.
AC Q8QP04;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (fragment).
GN AC1.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG-B11;
RA Ribeiro S.G., Ambrozovicus L.P., de Avila A.C., Calegario R.F.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RN in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY049208; AAL82833.1; -.
DR InterPro: IPR001191; Geminini AL1.
DR Pfam: PF00799; Geminini AL1; 1.
DR ProDom; PD000736; Geminini AL1; 1.
FT NON-TER 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BE0DD9C810 CRC64;

Query Match 74.88; Score 270; DB 12; Length 235;
Best Local Similarity 74.88; Pred. No. 1.9e-24;
Matches 50; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 4 WGFQVDRSARGCGCOTSDAAAEALNASSKEEALQIIAAAIPEKYLQFPHNLNSLDRI 63
Db 113 WGFQVDRSARGCGCQTANDAAAEALNASSKEEALQIIKEKLPKYLQFPHNLSCNLDRI 172

QY 64 DRIPDKTP 70
Db 173 DRIFSPPP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

```

```
RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126611; AAM95995.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF007799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 208 208
SQ SEQUENCE 208 AA; 23667 MW; 51211D58FAD690A6 CRC64;

Query Match 74.5%; Score 269; DB 12; Length 208;
Best Local Similarity 71.4%; Pred. No. 2.2e-24;
Matches 50; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 60
Db 110 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 169

QY 61 DRFDKTPPEP 70
Db 170 DRIFWKAPKP 179

RESULT 13
Q8JLY5 PRELIMINARY; PRT; 289 AA.
AC Q8JLY5;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;
RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126610; AAM95993.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF007799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 289 289
SQ SEQUENCE 289 AA; 32971 MW; 4ECF52F4C69C6764 CRC64;

Query Match 74.5%; Score 269; DB 12; Length 289;
Best Local Similarity 71.4%; Pred. No. 3.3e-24;
Matches 50; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 60
Db 110 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 169

QY 61 DRFDKTPPEP 70
Db 170 DRIFWKAPKP 179

RESULT 14
P88975 PRELIMINARY; PRT; 149 AA.
AC P88975;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
```

```
RN SEQUENCE FROM N.A.
RP STRAIN=Jamaican;
RA Roye M.E.;
RL Thesis (1996); Biochemistry, University of the West Indies, Jamaica.
DR EMBL; U75278; AAB36919.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF007799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16785 MW; E4CF5EED4C9CD508 CRC64;

Query Match 73.7%; Score 266; DB 12; Length 149;
Best Local Similarity 70.0%; Pred. No. 3.4e-24;
Matches 49; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 60
Db 52 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 111

QY 61 DRFDKTPPEP 70
Db 112 DRIFWKDPEP 121

RESULT 15
Q9YLA4 PRELIMINARY; PRT; 233 AA.
AC Q9YLA4;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica strain 1;
RA Roye M.E.;
RT "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Jamaica strain 1;
RC Roye M.E., McLaughlin W.A., Maxwell D.P.;
RT "Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098940; AAD17850.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF007799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 233 233
SQ SEQUENCE 233 AA; 26356 MW; AA490AF4D2166A02 CRC64;

Query Match 73.7%; Score 266; DB 12; Length 233;
Best Local Similarity 70.0%; Pred. No. 5.9e-24;
Matches 49; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 60
Db 110 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 169

QY 61 DRFDKTPPEP 70
Db 170 DRIFWKDPEP 179
```

Search completed: December 23, 2003, 09:03:35
Job time : 25.3333 secs

```

xx PA (UUNC-) UNIV NORTH CAROLINA STATE.
xx PI Hanley-Bowdoin L, Orozco BM, Kong L;
xx DR WPI; 2000-618851/59.
xx PT Transgenic plants with increased resistance to geminivirus infection
xx PT comprise a nucleic acid construct containing a nucleic acid sequence
xx PT encoding a mutant AL1 protein with a mutation in the Rb binding region
xx PS
xx PS Claim 52; Page 44; 73pp; English.
xx CC The present sequence represents a mutant peptide, derived from a
xx CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
xx CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
xx CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
xx CC protein are used to produce transgenic plants. The mutation in AL1 is
xx CC present in a ribosome binding region, and expression of mutant AL1
xx CC protein imparts increased resistance to geminivirus infection in the
xx CC plant. Mutant AL1 proteins are useful for producing plants having
xx CC increased resistance or reduced sensitivity to a geminivirus such as
xx CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
xx CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
xx CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
xx CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
xx CC virus, cotton leaf curl virus or beet curly top virus.
xx SQ Sequence 70 AA;
Query Match 100.0%; Score 359; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 5e-39;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDCRSARGCGQTSNDAAEALNASSKEEALQIIREKIPAAALQFHNLSNL 60
Db 1 TLVWGEFQVDCRSARGCGQTSNDAAEALNASSKEEALQIIREKIPAAALQFHNLSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 2
AAB18677
ID AAB18677 standard; peptide; 70 AA.
AC AAB18677;
XX
XX 22-JAN-2001 (first entry)
XX Peptide fragment from Rep protein of TGMV (amino acids 110-179).
XX DE
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS
XX OS Tomato golden mosaic virus.
XX PN WO200054573-Al.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-US06759.
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX PA (UUNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
xx PT Transgenic plants with increased resistance to geminivirus infection
xx PT comprise a nucleic acid construct containing a nucleic acid sequence
xx PT encoding a mutant AL1 protein with a mutation in the Rb binding region
xx PS
xx PS Disclosure; Page 18; 73pp; English.
xx CC The present sequence is derived from a geminivirus replication (Rep)
xx CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
xx CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
xx CC with other viral and host proteins. Mutants of the AL1 protein are used
xx CC to produce transgenic plants. The mutation in AL1 is present in a
xx CC ribosome binding region, and expression of mutant AL1 protein imparts
xx CC increased resistance to geminivirus infection in the plant. Mutant AL1
xx CC proteins are useful for producing plants having increased resistance or
xx CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
xx CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
xx CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
xx CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
xx CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
xx CC beet curly top virus.
xx SQ Sequence 70 AA;
Query Match 95.5%; Score 343; DB 21; Length 70;
Best Local Similarity 95.7%; Pred. No. 6.1e-37;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDCRSARGCGQTSNDAAEALNASSKEEALQIIREKIPAAALQFHNLSNL 60
Db 1 TLVWGEFQVDCRSARGCGQTSNDAAEALNASSKEEALQIIREKIPAAALQFHNLSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 3
AAB18687
ID AAB18687 standard; peptide; 356 AA.
XX
XX AC AAB18687;
XX
XX 22-JAN-2001 (first entry)
XX Amino acid sequence of a geminivirus replication protein of TGMV.
XX DE
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS
XX OS Tomato golden mosaic virus.
XX FH
XX FH Key Location/Qualifiers
XX FT Misc-difference 354
XX FT /note= "unspecified amino acid"
XX PN WO200054573-Al.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-US06759.
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX PA (UUNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
xx PT Transgenic plants with increased resistance to geminivirus infection

```


PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX
 PS Disclosure; Page 47-48; 73pp; English.
 XX
 CC The present sequence represents a geminivirus replication (Rep)
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
 CC catalyses cleavage and ligation of single-stranded DNA, and interacts
 CC with other viral and host proteins. Mutants of the AL1 protein are used
 CC to produce transgenic plants. The mutation in AL1 is present in a
 CC ribosome binding region, and expression of mutant AL1 protein imparts
 CC increased resistance to geminivirus infection in the plant. Mutant AL1
 CC proteins are useful for producing plants having increased resistance or
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 CC beet curly top virus.
 XX
 SQ Sequence 356 AA;

Query Match 95.5%; Score 343; DB 21; Length 356;
 Best Local Similarity 95.7%; Pred. No. 5.3e-36;
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDSARGGCGTSDNDAALNASSKEALQIREKIPAAALFQFHNLSNL 60
 DB 110 TLVWGFQVDSARGGCGTSDNDAALNASSKEALQIREKIPAAALFQFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 170 DRIFDKTPEP 179

RESULT 4
 AAB18685
 ID AAB18685 standard; peptide; 70 AA.
 XX
 AC AAB18685;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 10 /note= "wild type residue replaced with Ala"
 XX
 XX WO200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 XX
 XX 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 XX
 PS Claim 53; Page 46; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;

Query Match 93.3%; Score 335; DB 21; Length 70;
 Best Local Similarity 94.3%; Pred. No. 6.8e-36;
 Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDSARGGCGTSDNDAALNASSKEALQIREKIPAAALFQFHNLSNL 60
 DB 1 TLVWGFQVDSARGGCGTSDNDAALNASSKEALQIREKIPAAALFQFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70

RESULT 5
 AAB18688
 ID AAB18688 standard; peptide; 70 AA.
 XX
 AC AAB18688;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 19 /note= "wild type residue replaced with Ala"
 FT FT Misc-difference 20 /note= "wild type residue replaced with Ala"
 XX
 XX WO200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 XX
 XX 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX
 XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PS
 PS Disclosure; Page 48; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;

Query Match 92.5%; Score 332; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 1.7e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDSARGSCGTSNDAAAEALNASSKEEALQIIRKIPAAALFQPHNLSNL 60
 |||||
 Db 1 TLVWGFQVDSARGSCGTSNDAAAEALNASSKEEALQIIRKIPAAALFQPHNLSNL 60
 |||||
 QY 61 DRIFDKTPEP 70
 |||||
 Db 61 DRIFDKTPEP 70

RESULT 6
 AAB18692
 ID AAB18692 standard; peptide; 70 AA.
 AC AAB18692;
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 66 /note= "wild type residue replaced with Ala"
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 DR

PT Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PS
 PS Disclosure; Page 50; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 92.2%; Score 331; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 2.3e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDSARGSCGTSNDAAAEALNASSKEEALQIIRKIPAAALFQPHNLSNL 60
 |||||
 Db 1 TLVWGFQVDSARGSCGTSNDAAAEALNASSKEEALQIIRKIPAAALFQPHNLSNL 60
 |||||
 QY 61 DRIFDKTPEP 70
 |||||
 Db 61 DRIFDKTPEP 70

RESULT 7
 AAB18684
 ID AAB18684 standard; peptide; 70 AA.
 AC AAB18684;
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 7 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 DR

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 XX
 PS Claim 52; Page 45; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 91.6%; Score 329; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 4.1e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDSRGSGCQTSNDAAAEALNASSKEEALQIIRKIPAAALFQPHNLSNL 60
 DB 1 TLVWGEFQVDSRGSGCQTSNDAAAEALNASSKEEALQIIRKIPAAALFQPHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 8
 AAB18690
 ID AAB18690 standard; peptide; 70 AA.
 AC AAB18690;
 XX
 XX 22-JAN-2001 (first entry)
 DT
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 27 /note= "wild type residue replaced with Ala"
 FT Misc-difference 30 /note= "wild type residue replaced with Ala"
 FT Misc-difference 30 /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-A1.
 PN
 XX 21-SEP-2000.
 PD
 XX 15-MAR-2000; 2000WO-US06759.
 PF
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 PI
 XX

DR WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 XX
 PS Disclosure; Page 49; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 91.6%; Score 329; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 4.1e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDSRGSGCQTSNDAAAEALNASSKEEALQIIRKIPAAALFQPHNLSNL 60
 DB 1 TLVWGEFQVDSRGSGCQTSNDAAAEALNASSKEEALQIIRKIPAAALFQPHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 9
 AAB18678
 ID AAB18678 standard; peptide; 70 AA.
 AC AAB18678;
 XX
 XX 22-JAN-2001 (first entry)
 DT
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 12 /note= "wild type residue replaced with Ala"
 FT Misc-difference 13 /note= "wild type residue replaced with Ala"
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-A1.
 PN
 XX 21-SEP-2000.
 PD
 XX 15-MAR-2000; 2000WO-US06759.
 PF
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA

```

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX PA WPI; 2000-618851/59.
XX DR
XX XX Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT
XX PS Claim 53; Page 42-43; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 91.4%; Score 328; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 5.6e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 TLVWGEFQVDRSGRGCGQTNDAAAEALNASKEEALQIIREKIPAAALFQFHNLSNL 60
Db 1 TLVWGEFQVDRSGRGCGQTNDAAAEALNASKEEALQIIREKIPAAALFQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 10
AAB18686
ID AAB18686 standard; peptide; 70 AA.
AC AAB18686;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 24 /note= "wild type residue replaced with Leu"
XX Misc-difference 25 /note= "wild type residue replaced with Leu"
XX Misc-difference 26 /note= "wild type residue replaced with Leu"
XX
XX WO2000054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.

```

```

PR 09-APR-1999; 99US-0289346.
XX
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX FI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX XX Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT
XX PS Claim 53; Page 46; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 91.4%; Score 328; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 5.6e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 TLVWGEFQVDRSGRGCGQTNDAAAEALNASKEEALQIIREKIPAAALFQFHNLSNL 60
Db 1 TLVWGEFQVDRSGRGCGQTNDLLLEALNASKEEALQIIREKIPKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 11
AAB18689
ID AAB18689 standard; peptide; 70 AA.
AC AAB18689;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 22 /note= "wild type residue replaced with Ala"
XX Misc-difference 23 /note= "wild type residue replaced with Ala"
XX
XX WO2000054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX

```

```

PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
PS Disclosure; Page 48-49; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 91.1%; Score 327; DB 21; Length 70;
Best Local Similarity 92.9%; Pred. No. 7.5e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIREKIPAAALFQFHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIREKIPAAALFQFHNLSNL 60
OY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 12
AAB18680
ID AAB18680 standard; peptide; 70 AA.
XX
AC AAB18680;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
XX Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 42 /note= "wild type residue replaced with Ala"
FT Misc-difference 43 /note= "wild type residue replaced with Ala"
FT Misc-difference 44 /note= "wild type residue replaced with Ala"
XX
PN W0200054573-A1.
XX
PD 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
PS Claim 52; Page 43-44; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 90.5%; Score 325; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.4e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIREKIPAAALFQFHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIREKIPAAALFQFHNLSNL 60
OY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 13
AAB18691
ID AAB18691 standard; peptide; 70 AA.
XX
AC AAB18691;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
XX Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 34 /note= "wild type residue replaced with Ala"
FT Misc-difference 35 /note= "wild type residue replaced with Ala"
FT Misc-difference 36 /note= "wild type residue replaced with Ala"
XX
PN W0200054573-A1.
XX
PD 21-SEP-2000.

```

PN WO200054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI WPI; 2000-618951/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 XX Disclosure; Page 49; 73pp; English.
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA;
 SQ
 Query Match 90.5%; Score 325; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 1.4e-34;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDSARGCGCOTSDAAAEALNASSKEALQIIREKIPAAALFOFHNLSNL 60
 Db 1 TLVWGEFQVDSARGCGCOTSDAAAEALNASSKEALQIIREKIPAAALFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 Db 61 DRIFDKTPEP 70
 RESULT 14
 AAB18683
 ID AAB18683 standard; peptide; 70 AA.
 XX AAB18683;
 AC
 XX 22-JAN-2001 (first entry)
 DT Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 DE ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 KW Tomato golden mosaic virus.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 59 /note= "wild type residue replaced with Ala"
 FT Misc-difference 61 /note= "wild type residue replaced with Ala"
 FT

FT Misc-difference 62 /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-A1.
 PN 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI WPI; 2000-618951/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 XX Claim 53; Page 45; 73pp; English.
 PS The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA;
 SQ
 Query Match 89.4%; Score 321; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 4.5e-34;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDSARGCGCOTSDAAAEALNASSKEALQIIREKIPAAALFOFHNLSNL 60
 Db 1 TLVWGEFQVDSARGCGCOTSDAAAEALNASSKEALQIIREKIPAAALFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 Db 61 AAFDKTPEP 70
 RESULT 15
 AAB18682
 ID AAB18682 standard; peptide; 70 AA.
 XX AAB18682;
 AC
 XX 22-JAN-2001 (first entry)
 DT Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 DE ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 KW Tomato golden mosaic virus.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 52

FT /note= "wild type residue replaced with Ala"
FT Misc-difference 54
FT /note= "wild type residue replaced with Ala"
FT Misc-difference 55
FT /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX
XX (UYN-C-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
XX Claim 53; Page 44-45; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;

Query Match 88.9%; Score 319; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 8.3e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPAAALFOFHLNSNL 60
Db 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPAAALFOFHLNSNL 60
QY 61 DRIFDKTEEP 70
Db 61 DRIFDKTEEP 70


```
Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179

RESULT 2
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6
; Query Match 61.3%; Score 220; DB 3; Length 361;
; Best Local Similarity 58.6%; Pred. No. 3.7e-21;
; Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLWGFQVDGRSARGGQTSNDAAAEALNASSKEEALQIREKIPAAALFQPHNLNSNL 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179

RESULT 3
US-08-838-151A-6
; Sequence 6, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4
; Query Match 61.3%; Score 220; DB 3; Length 361;
; Best Local Similarity 58.6%; Pred. No. 3.7e-21;
; Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLWGFQVDGRSARGGQTSNDAAAEALNASSKEEALQIREKIPAAALFQPHNLNSNL 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179

RESULT 4
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6
; Query Match 61.3%; Score 220; DB 3; Length 361;
; Best Local Similarity 58.6%; Pred. No. 3.7e-21;
; Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLWGFQVDGRSARGGQTSNDAAAEALNASSKEEALQIREKIPAAALFQPHNLNSNL 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179
```

```
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6
; Query Match 61.3%; Score 220; DB 3; Length 361;
; Best Local Similarity 58.6%; Pred. No. 3.7e-21;
; Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLWGFQVDGRSARGGQTSNDAAAEALNASSKEEALQIREKIPAAALFQPHNLNSNL 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179

RESULT 4
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6
; Query Match 61.3%; Score 220; DB 3; Length 361;
; Best Local Similarity 58.6%; Pred. No. 3.7e-21;
; Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLWGFQVDGRSARGGQTSNDAAAEALNASSKEEALQIREKIPAAALFQPHNLNSNL 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179

RESULT 4
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6
; Query Match 61.3%; Score 220; DB 3; Length 361;
; Best Local Similarity 58.6%; Pred. No. 3.7e-21;
; Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLWGFQVDGRSARGGQTSNDAAAEALNASSKEEALQIREKIPAAALFQPHNLNSNL 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179
```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-8

Query Match 61.3%; Score 220; DB 3; Length 361;
Best Local Similarity 58.6%; Pred. No. 3.7e-21;
Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGTSDNAAEALNASSKEALQIIREKIPAAALFQPHNLNSL 60
DB 110 TLWGTQFQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLVHFNINSNL 169
QY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 5
US-08-809-103B-2
; Sequence 2, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-2

Query Match 61.0%; Score 219; DB 3; Length 359;
Best Local Similarity 58.0%; Pred. No. 5e-21;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
QY 2 LVWGEFQVDRSGRGCGTSDNAAEALNASSKEALQIIREKIPAAALFQPHNLNSLD 61
DB 111 LEWGTQFQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLVHFNINSLD 170
QY 62 RIFDKTPEP 70
DB 171 KVQVPPAP 179

RESULT 6
US-08-809-103B-4
; Sequence 4, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-4

Query Match 61.0%; Score 219; DB 3; Length 359;
Best Local Similarity 58.0%; Pred. No. 5e-21;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
QY 2 LVWGEFQVDRSGRGCGTSDNAAEALNASSKEALQIIREKIPAAALFQPHNLNSLD 61
DB 111 LEWGTQFQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLVHFNINSLD 170

Qy 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 7

US-08-809-103B-6
; Sequence 6, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-6

Query Match 61.0%; Score 219; DB 3; Length 359;
Best Local Similarity 58.0%; Pred. No. 5e-21;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
Qy 2 LVMGFEQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSLD 61
Db 111 LEWGTFFQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170

Qy 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 8

US-08-809-103B-8
; Sequence 8, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT

; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-8

Query Match 61.0%; Score 219; DB 3; Length 359;
Best Local Similarity 58.0%; Pred. No. 5e-21;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
Qy 2 LVMGFEQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSLD 61
Db 111 LEWGTFFQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170

Qy 62 RIFDKTPEP 70

Db 171 KVFQVPPAP 179

RESULT 9

US-08-838-151A-44
; Sequence 44, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geninivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-44

Query Match 60.7%; Score 218; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 6.7e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDRGARGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60
Db 110 TIWGFQVDRGARGGQSQSANDSYAKALNADSIESTILKEQPKDYVLQHNIRSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 11
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-49

Query Match 60.7%; Score 218; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 6.7e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDRGARGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60
Db 110 TIWGFQVDRGARGGQSQSANDSYAKALNADSIESTILKEQPKDYVLQHNIRSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 11
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

Query Match 60.7%; Score 218; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 6.7e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDRGARGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60
Db 110 TIWGFQVDRGARGGQSQSANDSYAKALNADSIESTILKEQPKDYVLQHNIRSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 11
US-08-838-151A-47
; Sequence 47, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-47

Query Match 60.7%; Score 218; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 6.7e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDRGARGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60
Db 110 TIWGFQVDRGARGGQSQSANDSYAKALNADSIESTILKEQPKDYVLQHNIRSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 11
US-08-838-151A-48
; Sequence 48, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-48

Query Match 60.7%; Score 218; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 6.7e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDRGARGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60
Db 110 TIWGFQVDRGARGGQSQSANDSYAKALNADSIESTILKEQPKDYVLQHNIRSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 11
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-49

Query Match 60.7%; Score 218; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 6.7e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDRGARGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60
Db 110 TIWGFQVDRGARGGQSQSANDSYAKALNADSIESTILKEQPKDYVLQHNIRSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179
```

```
Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 12
US-08-838-151A-52
; Sequence 52, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-52

Query Match 60.7%; Score 218; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 6.7e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSGRGCGQTSNDAAALNASSKEEALQIIRKIPAAALFQFHNLNSNL 60
Db 110 TIEWGQFQVDRSGRGCGQTSNDAAALNASSKEEALQIIRKIPAAALFQFHNLNSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 13
US-08-838-151A-55
; Sequence 55, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
```

```
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-55

Query Match 60.7%; Score 218; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 6.7e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSGRGCGQTSNDAAALNASSKEEALQIIRKIPAAALFQFHNLNSNL 60
Db 110 TIEWGQFQVDRSGRGCGQTSNDAAALNASSKEEALQIIRKIPAAALFQFHNLNSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 14
US-08-838-151A-24
; Sequence 24, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
```

```

; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-24

Query Match 56.5%; Score 203; DB 3; Length 357;
Best Local Similarity 65.6%; Pred. No. 6.8e-19;
Matches 40; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 4 WGEFQVDRGARGGCOTSDNDAAEALNASSKEEALQIIREKI PAAALFOFHNLSNLDRI 63
Db 111 FGVSQIDGRSARGGQQGNDAYALNAGSKSEALNLIKAPKDYILQFHNLSNLDRI 170

QY 64 F 64
Db 171 F 171

```

Search completed: December 23, 2003, 08:59:34
Job time : 12.6667 secs

```

RESULT 15
US-08-838-151A-27
; Sequence 27, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-27

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds
(without alignments)
172.015 Million cell updates/sec

Title: US-09-289-346B-5
Perfect score: 359
Sequence: 1 TLVWGFQVDSARGGCGT.....FOFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	359	100.0	70	10	US-09-289-346A-5
2	343	95.5	70	10	US-09-289-346A-1
3	343	95.5	356	10	US-09-289-346A-11
4	335	93.3	70	10	US-09-289-346A-9
5	332	92.5	70	10	US-09-289-346A-12
6	331	92.2	70	10	US-09-289-346A-16
7	329	91.6	70	10	US-09-289-346A-8
8	329	91.6	70	10	US-09-289-346A-14
9	328	91.4	70	10	US-09-289-346A-2
10	328	91.4	70	10	US-09-289-346A-10
11	327	91.1	70	10	US-09-289-346A-13
12	325	90.5	70	10	US-09-289-346A-4
13	325	90.5	70	10	US-09-289-346A-15
14	321	89.4	70	10	US-09-289-346A-7
15	319	88.9	70	10	US-09-289-346A-6

16	311	86.6	70	10	US-09-289-346A-3
17	66.5	18.5	512	12	US-10-301-661A-4
18	66.5	18.5	1217	15	US-10-156-761-13942
19	63.5	17.7	1713	15	US-10-171-311-113
20	62.5	17.4	429	12	US-10-032-585-7668
21	60.5	16.9	447	9	US-09-989-722-369
22	60.5	16.9	447	9	US-09-989-723-369
23	60.5	16.9	447	9	US-09-989-727-369
24	60.5	16.9	447	9	US-09-989-727-369
25	60.5	16.9	447	10	US-09-989-731-369
26	60.5	16.9	447	10	US-09-989-732-369
27	60.5	16.9	447	10	US-09-991-073-369
28	60.5	16.9	447	10	US-09-990-442-369
29	60.5	16.9	447	10	US-09-991-163-369
30	60.5	16.9	447	10	US-09-993-604-369
31	60.5	16.9	447	10	US-09-989-721-369
32	60.5	16.9	447	10	US-09-992-598-369
33	60.5	16.9	447	10	US-09-992-598-369
34	60.5	16.9	447	10	US-09-989-293A-369
35	60.5	16.9	447	10	US-09-989-735-369
36	60.5	16.9	447	10	US-09-990-444-369
37	60.5	16.9	447	10	US-09-991-181-369
38	60.5	16.9	447	10	US-09-989-730-369
39	60.5	16.9	447	10	US-09-990-436-369
40	60.5	16.9	447	10	US-09-993-687-369
41	60.5	16.9	447	11	US-09-989-734-369
42	60.5	16.9	447	11	US-09-997-653-369
43	60.5	16.9	447	11	US-09-993-667-369
44	60.5	16.9	447	11	US-09-997-428-369
45	60.5	16.9	447	11	US-09-997-666-369

ALIGNMENTS

RESULT 1
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US2002013867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence. Fragment of TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (EKY159->AAA159).
US-09-289-346A-5

Query Match	100.0%	Score	359	DB	10	Length	70
Best Local Similarity	100.0%	Pred. No.	1.6e-39	Indels	0	Gaps	0
Matches	70	Conservative	0	Mismatches	0		
Qy	1	TLVWGFQVDSARGGCGT	SNDAAAEALNASSKEBALQIIRKIPAAALFQPHNLNSL	60			
Db	1	TLVWGFQVDSARGGCGT	SNDAAAEALNASSKEBALQIIRKIPAAALFQPHNLNSL	60			
Qy	61	DRIFDKTPEP	70				

```
Db      61 DRIFDKTPEP 70
|||||
110 TLVWGEFQVGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSL 169

RESULT 4
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match      93.3%; Score 335; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 2.2e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 TLVWGEFQVGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPAAALQFPHNLNSL 60
|||||
Db      1 TLVWGEFQVGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSL 60

Qy      61 DRIFDKTPEP 70
|||||
Db      61 DRIFDKTPEP 70

RESULT 5
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12

Query Match      92.5%; Score 332; DB 10; Length 70;

Db      61 DRIFDKTPEP 70
|||||
110 TLVWGEFQVGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSL 169

RESULT 2
US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1

Query Match      95.5%; Score 343; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 2e-37; 3; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 TLVWGEFQVGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPAAALQFPHNLNSL 60
|||||
Db      1 TLVWGEFQVGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSL 60

Qy      61 DRIFDKTPEP 70
|||||
Db      61 DRIFDKTPEP 70

RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match      95.5%; Score 343; DB 10; Length 356;
Best Local Similarity 95.7%; Pred. No. 1.7e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 TLVWGEFQVGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPAAALQFPHNLNSL 60
|||||
```



```
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQI18->AAI18).
US-09-289-346A-8

Query Match          91.6%; Score 329; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFOFHNLSNL 60
   |||||
Db 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFOFHNLSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 6
US-09-289-346A-16
; Sequence 16, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-16

Query Match          92.2%; Score 331; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 7.5e-36;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFOFHNLSNL 60
   |||||
Db 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFOFHNLSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 7
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
```

```
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQI18->AAI18).
US-09-289-346A-8

Query Match          91.6%; Score 329; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFOFHNLSNL 60
   |||||
Db 1 TLVWGEAAVDGRSARGGCQTSDNDAALNASSKEALQIIREKIPKYLFOFHNLSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 8
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match          91.6%; Score 329; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFOFHNLSNL 60
   |||||
Db 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPKYLFOFHNLSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 9
US-09-289-346A-2
; Sequence 2, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
```

```
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
US-09-289-346A-2

Query Match          91.4%; Score 328; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.9e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 60
Db 1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLQFHNLNSNL 60

QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LLLL136).
US-09-289-346A-10

Query Match          91.4%; Score 328; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.9e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 60
Db 1 TLVWGEFQVDRSARGCGCQTSNDLLLEALNASSKEEALQIIREKIPKYLQFHNLNSNL 60

QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
```

```
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-13

Query Match          91.1%; Score 327; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.5e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 60
Db 1 TLVWGEFQVDRSARGCGCQTSAAAAAEALNASSKEEALQIIREKIPKYLQFHNLNSNL 60

QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (42)..(44)
; OTHER INFORMATION: Description of Artificial sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAA154).
US-09-289-346A-4

Query Match          90.5%; Score 325; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 4.6e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 60
Db 1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEEALQIAAAIPEKYLQFHNLNSNL 60

QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al., 346A
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match      90.5%; Score 325; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. NO. 4.6e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQPHNLNSNL 60
Db 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSAAALQIIREKIPKYLQPHNLNSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 14
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDRI172->ALAA172).
US-09-289-346A-7

Query Match      89.4%; Score 321; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. NO. 1.5e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQPHNLNSNL 60
Db 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPKYLQPHNLNSAL 60
QY 61 DRIFDKTPEP 70
Db 61 AAIFDKTPEP 70

; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al., 346A
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-6

Query Match      88.9%; Score 319; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. NO. 2.8e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQPHNLNSNL 60
Db 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPKYLQPHNLNSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

Search completed: December 23, 2003, 09:43:29
Job time : 76 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds
(without alignments)
673.181 Million cell updates/sec

Title: US-09-289-346B-5

Perfect score: 359

Sequence: 1 TLVWGFQVDRSARGGCT.....FQFHNLSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	343	95.5	352	1 QOCVLI	Al1 protein - toma
2	247	68.8	361	1 QOCVPT	Al1 protein - toma
3	243	67.7	358	2 S07594	hypothetical prote
4	232	64.6	362	1 JQ1887	Al1 protein - toma
5	226	63.0	359	2 S39211	gene Cl protein -
6	224	62.4	349	2 JQ2300	replicase - pepper
7	224	62.4	349	2 S31875	Al1 protein - pepp
8	219	61.0	359	2 S22593	hypothetical prote
9	216	60.2	351	2 JQ2327	Al1 protein - Indi
10	216	60.2	358	1 JQ1870	Al1 protein - toma
11	215	59.9	355	1 QOCVW1	AV1 protein - abut
12	213	59.3	359	2 S39235	gene Cl protein -
13	212	59.1	385	2 S28360	Al1 protein - beet
14	209	58.2	360	2 S59885	replication-associ
15	203	56.5	357	1 QOCVC1	Al1 protein - toma
16	134	37.3	131	2 S45059	AC1 protein (clone
17	118	32.9	347	1 QOCVU1	Al1 protein - squa
18	85	18.1	587	2 JCL1419	Fc gamma (IgG) rec
19	63.5	17.7	1033	2 E97700	hypothetical prote
20	63.5	17.7	1713	2 A55347	adhesive ligand ep
21	62.5	17.4	642	2 D90558	topoisomerase iv s
22	62	17.3	160	2 G82060	hypothetical prote
23	62	17.3	308	2 E86840	protein maturation
24	61.5	17.1	300	2 G89582	protein K07E3.3 [i
25	61.5	17.1	538	2 AD0285	probable periplasm
26	61	17.0	631	2 S36505	R1 protein - human
27	61	17.0	840	2 T36175	probable large ATP
28	60.5	16.9	338	2 AG3582	iron(III)-binding
29	60.5	16.9	429	2 A44384	GTP-binding regula

30 60.5 16.9 435 2 E59096 hypothetical prote
31 60.5 16.9 447 2 T12544 hypothetical prote
32 60.5 16.9 1070 1 A54600 1-phosphatidylinos
33 60 16.7 397 2 B71078 probable NADH oxid
34 60 16.7 714 2 C95382 probable ferrichro
35 59.5 16.6 706 2 H71707 hypothetical prote
36 59.5 16.6 1053 2 T06483 probable ubiquitin
37 59.5 16.6 1610 2 A46227 voltage-dependent
38 59.5 16.6 1646 2 JH0422 voltage-dependent
39 59.5 16.6 2137 2 T05244 hypothetical prote
40 59.5 16.6 2161 2 JH0564 hypothetical prote
41 59.5 16.6 2181 2 A38198 calcium channel al
42 59.5 16.6 2203 2 T42742 voltage-dependent
43 59 16.4 351 2 AF2626 hypothetical prote
44 59 16.4 351 2 E97408 fbpa (AR006039) [i
45 59 16.4 451 2 S26839 retrovirus-related

ALIGNMENTS

RESULT 1

QOCVLI

Al1 protein - tomato golden mosaic virus

C:Species: tomato golden mosaic virus

A:Note: host Nicotiana sp. (tobacco)

C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994

C:Accession: A04170

R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.

EMBO J. 3, 2197-2205, 1984

A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomato

A:Reference number: A04163

A:Accession: A04170

A:Molecule type: DNA

A:Residues: 1-352 <HAM>

C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A

C:Genetics:

A:Map position: segment A

C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 95.5%; Score 343; DB 1; Length 352;
Best Local Similarity 95.7%; Pred. NO. 1.6e-31;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSARGGCTSDNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60
DB 111 TLVWGFQVDRSARGGCTSDNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 170

QY 61 DRIFDKTPPEP 70

DB 171 DRIFDKTPPEP 180

RESULT 2

QOCVPT

Al1 protein - potato yellow mosaic virus (isolate Venezuela)

C:Species: potato yellow mosaic virus

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000

C:Accession: JU0364

R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.

J. Gen. Virol. 72, 1515-1520, 1991

A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yell

A:Reference number: JU0362; MUID:91311403; PMID:1856690

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-361 <COU>

A:Cross-references: GB:D00940; NID:G222458; PIDN:BAA00782.1; PID:G222459

C:Genetics:

A:Map position: segment A

C:Superfamily: tomato golden mosaic virus Al1 protein

S39235
gene C1 protein - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
C:Accession: S39235
R:Crepi, S.; Noris, E.; Vaira, A.; Bosco, D.; Accotto, G.
submitted to the EMBL Data Library, December 1993
A:Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.
A:Reference number: S39233
A:Accession: S39235
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <CRE>
A:Cross-references: EMBL:Z28390; NID:g1041671; PID:gl334964
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.3%; Score 213; DB 2; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.2e-16;
Matches 39; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 2 LVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQFHNLNSNLD 61
Db 111 LEWGTTFIDGRSARGGCGTANDAYAKAINRSKSEALDVIKQLAPRDYVLHFHNISNLD 170

Qy 62 RIFDKTPEP 70
Db 171 KVFOVPPAP 179

RESULT 13
S28360
AL1 protein - beet curly top virus
C:Species: beet curly top virus
C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Sep-1999
C:Accession: S28360
R:Stanley, J.; Markham, P.G.; Callis, R.J.; Pinner, M.S.
EMBO J. 5, 1761-1767, 1986
A:Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly top
A:Reference number: S28360
A:Accession: S28360
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-385 <STA>
A:Cross-references: GB:M24597; EMBL:X04144; NID:g210678; PIDN:AAA42751.1; PID:g210679
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.1%; Score 212; DB 2; Length 385;
Best Local Similarity 55.7%; Pred. No. 1.7e-16;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQFHNLNSNL 60
Db 137 TIEWGEFIDGRSARGGCGTANDSVAKALNATSLDQALQILKEQPKDYFLQHHNLNNA 196

Qy 61 DRIFDKTPEP 70
Db 197 QKIFQRPDP 206

RESULT 14
S59885
replication-associated protein C1 - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C>Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
C:Accession: S59885
R:Hong, Y.; Harrison, B.D.
submitted to the EMBL Data Library, February 1995
A:Description: Nucleotide sequences from tomato leaf curl viruses from different countries
d geminiviruses.
A:Reference number: S58346
A:Accession: S59885
A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-360 <HON>
A:Cross-references: EMBL:Z48182; NID:g944838; PIDN:CAA88229.1; PID:g974211
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 58.2%; Score 209; DB 2; Length 360;
Best Local Similarity 62.1%; Pred. No. 3.5e-16;
Matches 41; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 4 WGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQFHNLNSNLDRI 63
Db 113 FGVFQIDGRSARGGCGQSANDAYAEALNSGSKAAALJILREKAPKDPVLOFHNLSNLDRI 172

Qy 64 FDKTPE 69
Db 173 FTPEAE 178

RESULT 15
QQCVCI
AL1 protein - tomato yellow leaf curl virus
N:Alternate names: C1 protein
C:Species: tomato yellow leaf curl virus
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: D40779
R:Navot, N.; Fichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.
Virology 185, 151-161, 1991
A:Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single
A:Reference number: A40779; MUID:92024070; PMID:1926771
A:Accession: D40779
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-357 <NAV>
A:Cross-references: GB:X15656; NID:g62204; PIDN:CAA33688.1; PID:g62207
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 56.5%; Score 203; DB 1; Length 357;
Best Local Similarity 65.6%; Pred. No. 1.7e-15;
Matches 40; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 4 WGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQFHNLNSNLDRI 63
Db 111 FGVSQIDGRSARGGCGQSANDAYAEALNSGSKSEALNLIKKEAPKDYILOFHNLSNLDRI 170

Qy 64 F 64
Db 171 F 171

Search completed: December 23, 2003, 09:05:21
Job time : 11 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.7778 Seconds
(without alignments)
569.747 Million cell updates/sec

Title: US-09-289-346b-5
Perfect score: 359
Sequence: 1 TLVWGEFQVDRSARGGCQT.....FOFHLNSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	343	95.5	352	1	VAL1_TGMV	P03567 tomato gold
2	247	68.8	361	1	VAL1_PYMV	P27258 potato yell
3	243	67.7	358	1	VAL1_CLVK	P14982 cassava lat
4	243	67.7	358	1	VAL1_CLVN	P14972 cassava lat
5	232	64.6	362	1	VAL1_TYLCU	P36279 tomato yell
6	226	63.0	359	1	VAL1_TYLCU	P38609 tomato yell
7	224	62.4	349	1	VAL1_PHVU	O06923 pepper huas
8	219	61.0	359	1	VAL1_TYLCM	P27260 tomato yell
9	216	60.2	353	1	VAL1_BGMV	P05175 bean golden
10	216	60.2	361	1	VAL1_TMOV	O06657 tomato mott
11	215	59.9	355	1	VAL1_ABMVW	P21947 abutilon mo
12	212	59.1	358	1	VAL1_BCTV	P14991 beet curly
13	203	56.5	357	1	VAL1_TYLCV	P27259 tomato yell
14	118	32.9	347	1	VAL1_SLVC	P29048 squash leaf
15	65	18.1	630	1	VE1_HPV66	O80957 human papil
16	64.5	18.0	298	1	OLG2_CHICK	O90xb3 gallus gall
17	63.5	17.7	298	1	LNA3_HUMAN	O16787 homo sapien
18	62.5	17.4	428	1	G8A1_CANAL	P28868 candida alb
19	61.5	17.1	476	1	DGRE_HUMAN	O96df8 homo sapien
20	61.5	17.1	479	1	DGRE_MOUSE	O70279 mus musculus
21	61	17.0	631	1	VE1_HPV30	O05112 human papil
22	60.5	16.9	447	1	TRL2_HUMAN	O944p3 homo sapien
23	60.5	16.9	1070	1	P11B_HUMAN	P42338 homo sapien
24	59.5	16.6	706	1	Y006_RICPR	Q9zed6 rickettsia
25	59.5	16.6	1053	1	UBA3_WHEAT	P31252 triticum ae
26	59.5	16.6	1610	1	CCAD_MESAU	Q09244 mesocricetu
27	59.5	16.6	2161	1	CCAD_HUMAN	O01668 homo sapien
28	59.5	16.6	2203	1	CCAD_RAT	P27732 rattus norv
29	59	16.4	703	1	GYS2_RAT	P17625 rattus norv
30	59	16.4	1852	1	CCAS_CYPCA	P22316 cyprinus ca
31	58	16.2	387	1	Y4PF_RHISN	P55615 rhizobium s
32	58	16.2	1127	1	Y855_TREPA	O83827 treponema p
33	58	16.2	1608	1	HLVA_SERMA	P15320 serrattia ma

ALIGNMENTS

RESULT 1

ID	VAL1_TGMV	STANDARD;	PRT;	352 AA.
AC	P03567;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-JUN-1994 (Rel. 29, Last annotation update)			
DE	AL1 protein.			
GN	AC1.			
OS	Tomato golden mosaic virus (TGMV).			
OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.			
OX	NCBI_TaxID=10831;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;			
RT	*Complete nucleotide sequence of the infectious cloned DNA components			
RT	of tomato golden mosaic virus: potential coding regions and regulatory			
RT	sequences. #;			
RL	EMBO J. 3:2197-2205(1984).			
CC	-1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
EMBL;	K02029; -; NOT_ANNOTATED_CDS.			
DR	PIR; A04170; QOCVLL.			
DR	InterPro; IPR001191; Gemini_AL1.			
DR	Pfam; PF00799; Gemini_AL1.			
DR	PRINTS; PR00227; GEMCOATALL.			
DR	ProDom; PD000736; Gemini_AL1; 1.			
KW	ATP-binding.			
FT	NP_BIND 223 230 ATP (POTENTIAL).			
SQ	SEQUENCE 352 AA; 40332 MW; C33C938E9644B44 CRC64;			
Query Match	95.5%; Score 343; DB 1; Length 352;			
Best Local Similarity	95.7%; Pred. No. 6.1e-32;			
Matches	67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Qy	1 TLVWGEFQVDRSARGGCQTSNDAAALNASSKEEALQITREKIPAAALQFHLNSNL 60			
Db	111 TLVWGEFQVDRSARGGCQTSNDAAALNASSKEEALQITREKIPKYLEFQFHLNSNL 170			
Qy	61 DRIEDKTPPEP 70			
Db	171 DRIEDKTPPEP 180			
RESULT 2				
VAL1_PYMV				
ID	VAL1_PYMV	STANDARD;	PRT;	361 AA.
AC	P27258;			


```
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; D00940; BAA00782.1; -.
DR PIR; J00364; QOCVPT.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;

Query Match 68.8%; Score 247; DB 1; Length 361;
Best Local Similarity 68.1%; Pred. No. 6.5e-21;
Matches 47; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRGARGCGQTSNDAAAEALNASSKEALQIIREKIPAAALFQPHNLNSNL 60
Db 110 TIEWGLFQIDGRSARGGQQTVDAAAEALNKGKTKKAEAMKIKKLEKFLFQVHNLSCNL 169

QY 61 DRIFDKTPE 69
Db 170 DRIFDKAPE 178

RESULT 3
VAL1_CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN ACl.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA."
RL Nature 301:260-262(1983).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
```

```
CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753BE92D69 CRC64;

Query Match 67.7%; Score 243; DB 1; Length 358;
Best Local Similarity 64.3%; Pred. No. 1.8e-20;
Matches 45; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRGARGCGQTSNDAAAEALNASSKEALQIIREKIPAAALFQPHNLNSNL 60
Db 109 TIEWGQFQIDGRSARGGQGSANDAYAKALNKGKSEALNVIRELVKDFVLQFPHNLNSNL 168

QY 61 DRIFDKTPE 70
Db 169 DRIFQEPFAP 178

RESULT 4
VAL1_CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN ACl.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain)."
RL Nucleic Acids Res 18:197-198(1990).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; X17095; CAA34953.1; -.
DR PIR; S07594; S07594.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16BB0CB2D5E2C CRC64;

Query Match 67.7%; Score 243; DB 1; Length 358;
Best Local Similarity 64.3%; Pred. No. 1.8e-20;
Matches 45; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRGARGCGQTSNDAAAEALNASSKEALQIIREKIPAAALFQPHNLNSNL 60
Db 109 TIEWGQFQIDGRSARGGQGSANDAYAKALNKGKSEALNVIRELVKDFVLQFPHNLNSNL 168

QY 61 DRIFDKTPE 70
Db 169 DRIFQEPFAP 178
```

```
-----
CC EMBL; Z25751; CAA81026.1; -.
DR PIR; S39211; S39211.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3BC CRC64;

Query Match 63.0%; Score 226; DB 1; Length 359;
Best Local Similarity 60.9%; Pred. No. 1.7e-18;
Matches 42; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 2 LVMGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQPHNLNSLD 61
Db 111 LEMGTFQIDGRSARGGQGTANDAYAKAINAGSKSEALDVIKELAPRDVYLHFFHNSLD 170

QY 62 RIFDKTPEP 70
Db 171 RVFQVPPAP 179

RESULT 7
VAL1_TYLCU STANDARD; PRT; 349 AA.
ID VAL1_TYLCU STANDARD; PRT; 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AL1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
RT comparison with bipartite geminiviruses.";
RL J. Gen. Virol. 74:2225-2231(1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; X70418; CAA49856.1; -.
DR PIR; JQ2300; JQ2300.
DR PIR; S31875; S31875.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 39722 MW; D5F4E76CD56370F4 CRC64;

Query Match 62.4%; Score 224; DB 1; Length 349;
Best Local Similarity 61.4%; Pred. No. 2.7e-18;
Matches 43; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQPHNLNSLD 60
Db 110 TVWGEFQIDGRSARGGQGSANDTYAKALNSAAEALQIKEQPFQHFLOFHNVSNA 169

-----
RESULT 5
VAL1_TYLCU STANDARD; PRT; 362 AA.
ID VAL1_TYLCU STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Rigden J.E., Krake L.R., Mullineaux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
RT geminivirus.";
RL J. Gen. Virol. 74:147-151(1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR PIR; JQ1887; JQ1887.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 64.6%; Score 232; DB 1; Length 362;
Best Local Similarity 55.3%; Pred. No. 3.4e-19;
Matches 47; Conservative 8; Mismatches 14; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQPHNLNSLD 60
Db 110 TLEWGEFQIDGRSARGGQGSANDAYAKALNTGSKSEALNVRELAPKDVVLQFPHNLNSLD 169

QY 61 DRI-----FKTPE 69
Db 170 DRIPTPLEVYVSPFLSSFDVRPE 194

RESULT 6
VAL1_TYLCU STANDARD; PRT; 359 AA.
ID VAL1_TYLCU STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Noris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
RT from the west Mediterranean basin: the nucleotide sequence of an
RT infectious clone from Spain.";
RL Arch. Virol. 135:165-170(1994).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

```

QY 61 DRIFDKTPEP 70
DB 170 NRIFQTPPEP 179

RESULT 8
VAL1_TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE A11 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP MEDLINE=92107660; PubMed=1840676;
RA Kheyr-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RA "Tomato yellow leaf curl virus from Sardinia is a
RT whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M10070; AAA46318.1; -
DR InterPro; IPR001191; Gemini_A11.
DR Pfam; PF00799; Gemini_A11; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_A11; 1.
DR ATP-binding.
KW NP BIND 220 229 ATP (POTENTIAL).
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 60.2%; Score 216; DB 1; Length 353;
Best Local Similarity 60.0%; Pred. No. 2.3e-17;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGGCGTSDAAAEALNAGSKKEALQIIREKIPAAALFQFHNLNSNL 60
DB 110 TLVWGFQVDGRSARGGCGTSDAAAEALNAGSKKEALQIIREKIPAAALFQFHNLNSNL 169
QY 61 DRIFDKTPEP 70
DB 170 ERIFFKVPEP 179

RESULT 10
VAL1_TMOV STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE A11 protein.
GN A11.
OS Tomato mottle virus (isolate Florida) (TMOV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93107856; PubMed=1469361;
RA Abouzid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida.";
RL J. Gen. Virol. 73:3225-3229(1992).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L14460; AAC32414.1; -
DR PIR; JQ1870; JQ1870.
DR InterPro; IPR001191; Gemini_A11.
DR Pfam; PF00799; Gemini_A11; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_A11; 1.
KW ATP-binding.

QY 2 LVWGFQVDGRSARGGCGTSDAAAEALNAGSKKEALQIIREKIPAAALFQFHNLNSNL 61
DB 111 LVWGFQVDGRSARGGCGTSDAAAEALNAGSKKEALQIIREKIPAAALFQFHNLNSNL 170
QY 62 RIFDKTPEP 70
DB 171 KVQFQVPPAP 179

RESULT 9
VAL1_BGMV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE A11 protein (40.2 kDa protein).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]

```

```
FT NP_BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 8138B65CERAC6950 CRC64;

Query Match 60.2%; Score 216; DB 1; Length 361;
Best Local Similarity 57.1%; Pred. No. 2.3e-17;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAARALNASSKEALQIIREKIPAAALFQPHNLNSL 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TLWGEFQIDGRSARGGQSDNSYAKALNAGVSQALAVLREBQPKDFVLQHNIRSL 169
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DRIFDKTPEP 70
   :|||:|||||
Db 170 ERIFAKAPEP 179
   :|||:|||||

RESULT 11
VAL1_ABMVW
ID VAL1_ABMVW STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
SQ SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimmat G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
   as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation -
   the European Bioinformatics Institute. There are no restrictions on its
   use by non-profit institutions as long as its content is in no way
   modified and this statement is not removed. Usage by and for commercial
   entities requires a license agreement (See http://www.isb-sib.ch/announce/
   or send an email to license@isb-sib.ch).
CC
CC EMBL; X04144; -; NOT ANNOTATED_CDS.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 222 228 ATP (POTENTIAL).
SQ SEQUENCE 355 AA; 40257 MW; 16A2CABA63251E95 CRC64;

Query Match 59.9%; Score 215; DB 1; Length 355;
Best Local Similarity 58.6%; Pred. No. 3e-17;
Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAARALNASSKEALQIIREKIPAAALFQPHNLNSL 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TAEWGEFQIDGRSARGGQSDNSYAKALNAGDVQSALNILEEQPKDFVLQHNIRSL 169
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DRIFDKTPEP 70
   :|||:|||||
Db 170 ERIFAKAPEP 179
   :|||:|||||

RESULT 12
VAL1_BCTV
ID VAL1_BCTV STANDARD; PRT; 358 AA.
AC P14991;
DT 01-APR-1990 (Rel. 14, Created)
```

```
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein (40.8 kDa protein).
OC Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
SQ SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
   beet curly top virus.";
RL EMBO J. 5:1761-1767(1986).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation -
   the European Bioinformatics Institute. There are no restrictions on its
   use by non-profit institutions as long as its content is in no way
   modified and this statement is not removed. Usage by and for commercial
   entities requires a license agreement (See http://www.isb-sib.ch/announce/
   or send an email to license@isb-sib.ch).
CC
CC EMBL; X04144; -; NOT ANNOTATED_CDS.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match 59.1%; Score 212; DB 1; Length 358;
Best Local Similarity 55.7%; Pred. No. 6.6e-17;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAARALNASSKEALQIIREKIPAAALFQPHNLNSL 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TIWGEFQIDGRSARGGQSDNSYAKALNATSLDQALILKEEQPKDFVLQHNILNNA 169
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DRIFDKTPEP 70
   :|||:|||||
Db 170 QKIFQRPDP 179
   :|||:|||||

RESULT 13
VAL1_TYLCV
ID VAL1_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
SQ SEQUENCE FROM N.A.
RX MEDLINE=92024070; PubMed=1926771;
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
   with a single genomic component.";
RL Virology 185:151-161(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation -
   the European Bioinformatics Institute. There are no restrictions on its
   use by non-profit institutions as long as its content is in no way
   modified and this statement is not removed. Usage by and for commercial
   entities requires a license agreement (See http://www.isb-sib.ch/announce/
   or send an email to license@isb-sib.ch).
CC
```

```
DR EMBL; X15656; CAA33688.1; --
DR FIR; D40779; QOCVCL; Gemini_AL1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 219 226 ATP (POTENTIAL).
SQ SEQUENCE 357 AA; 40678 MW; 939AB681A3B2A7 CRC64;

Query Match 56.5%; Score 203; DB 1; Length 357;
Best Local Similarity 65.6%; Pred. No. 7.1e-16;
Matches 40; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 4 WGFQVDGRSARGCGCOTSDNDAAEALNASSKEALQIIREKIPAAALFOFHNLNSLDRIF 63
Db 111 FGVSQIDGRSARGGQSQANDAYAEALNSGSKSEALNIKERKPKDYILQFHNLSSLDRIF 170

QY 64 F 64
Db 171 F 171

RESULT 14
VAL1 SLCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE A11 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G., Laxdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype.";
RL Virology 180:58-69(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M38183; AAC32410.1; ALT_INIT.
DR FIR; C36785; QOCVSL.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDABDDDEL22110E CRC64;

Query Match 32.9%; Score 118; DB 1; Length 347;
Best Local Similarity 37.9%; Pred. No. 3.9e-06;
Matches 25; Conservative 12; Mismatches 25; Indels 4; Gaps 1;

QY 5 GEFQVDGRSARGCGCOTSDNDAAEALNASSKEALQIIREKIPAAALFOFHNLNSLDRIF 64
Db 116 GQYKVSQ-----GSKSNKDDVYHNAYNAGSAGEALDIIRKAGDPKTFIVYHNHLLANVERLF 171

QY 65 DKTPRP 70
Db 172 QKPPRP 177
```

RESULT 15

```
VE1_HPV66 STANDARD; PRT; 630 AA.
ID VE1_HPV66
AC Q80957;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Replication protein E1.
GN E1.
OS Human papillomavirus type 66.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=371119;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U31794; AAA79501.1; -.
DR InterPro; IPR001177; Papillom_E1.
DR Pfam; PF00519; E1; 1.
DR Pfam; PF00524; E1_N; 1.
KW Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
KW Nuclear protein.
FT NP_BIND 458 465 ATP (POTENTIAL).
SQ SEQUENCE 630 AA; 72065 MW; 22DDDA5934F7291B CRC64;

Query Match 18.1%; Score 65; DB 1; Length 630;
Best Local Similarity 25.5%; Pred. No. 9.3;
Matches 13; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 19 QTSNDAAAEALNASSKEALQIIREKIPAAALFOFHNLNSLDRIFDKTPE 69
Db 269 KITTKSLSSILNVQEQMLIQPKLRSPAVALYFYKTAMSNISEVYGETPE 319
```

Search completed: December 23, 2003, 08:57:38

Job time : 5.77778 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: December 23, 2003, 08:51:23 ; Search time 25.3333 Seconds
(without alignments)
713.040 Million cell updates/sec

Title: US-09-289-346B-5
Perfect score: 359
Sequence: 1 TLVWGEFQDGRSARGGQCT.....FOFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525
Minimum DB seq length: 0
Maximum Match 100%
Listing first 45 summaries
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	298	83.0	351	Q91R10	Q91R10 tomato seve
2	296	82.5	352	Q9E000	Q9E000 tomato rugo
3	288	80.2	232	Q8QPV3	Q8QPV3 tomato chlo
4	287	79.9	226	Q9WHF6	Q9WHF6 tomato mild
5	277	77.2	361	Q67574	Q67574 bean golden
6	275	76.6	225	Q9QDB1	Q9QDB1 cowpea gold
7	275	76.6	226	Q09727	Q09727 leonurus mo
8	271	75.5	185	Q98693	Q98693 sida golden
9	271	75.5	314	Q9ELT8	Q9ELT8 sweet potat
10	271	75.5	364	Q9QS55	Q9QS55 sweet potat
11	268	74.7	235	Q9QPU4	Q9QPU4 tomato infe
12	267	74.4	208	Q8JLY3	Q8JLY3 potato yell
13	267	74.4	289	Q8JLY5	Q8JLY5 potato yell
14	264	73.5	149	P88975	P88975 macroptiliu
15	264	73.5	190	Q9Z089	Q9Z089 tobacco lea
16	264	73.5	190	Q9Z084	Q9Z084 tobacco lea

17	264	73.5	233	12	Q9YLA4	Q9YLA4 macroptiliu
18	263	73.3	190	12	Q9W827	Q9W827 tobacco lea
19	263	73.3	208	12	Q9Z0C4	Q9Z0C4 tobacco lea
20	263	73.3	359	12	Q91M88	Q91M88 tobacco lea
21	263	73.3	359	12	Q8TV88	Q8TV88 tomato curl
22	263	73.3	361	12	Q8TMJ4	Q8TMJ4 potato yell
23	261	72.7	208	12	Q9Z0C0	Q9Z0C0 tobacco lea
24	261	72.7	208	12	Q9Z0B8	Q9Z0B8 tobacco lea
25	259	72.1	208	12	Q9Z0B6	Q9Z0B6 tobacco lea
26	259	72.1	361	12	Q8QVH0	Q8QVH0 ageratum en
27	258	71.9	203	12	Q9Z083	Q9Z083 tobacco lea
28	258	71.9	234	12	Q9Z180	Q9Z180 geminivirid
29	257	71.6	360	12	Q8QMH4	Q8QMH4 sida mottie
30	256	71.3	223	12	Q8QPU7	Q8QPU7 tomato seve
31	251	69.9	208	12	Q9Z0A0	Q9Z0A0 tobacco lea
32	251	69.9	363	12	Q72719	Q72719 cotton leaf
33	251	69.9	363	12	Q72705	Q72705 cotton leaf
34	250	68.6	190	12	Q9Z086	Q9Z086 tobacco lea
35	250	69.6	208	12	Q9Z0C6	Q9Z0C6 tobacco lea
36	249	69.4	349	12	Q88888	Q88888 tomato pseu
37	249	69.4	363	12	Q73577	Q73577 cotton leaf
38	249	69.4	364	12	Q8V524	Q8V524 ipomoea lea
39	248	69.1	359	12	Q91B86	Q91B86 ageratum ye
40	248	69.1	360	12	Q9DX10	Q9DX10 ageratum ye
41	247	68.8	348	12	Q911W5	Q911W5 macroptiliu
42	246	68.5	190	12	Q9Z0A7	Q9Z0A7 tobacco lea
43	246	68.5	362	12	Q8V016	Q8V016 cotton leaf
44	246	68.5	362	12	Q8V018	Q8V018 cotton leaf
45	246	68.5	362	12	Q8V618	Q8V618 cotton leaf

ALIGNMENTS

RESULT 1
Q91R10 PRELIMINARY; PRT; 351 AA.
ID Q91R10
AC Q91R10;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Rep protein.
GN AC1.

OS Tomato severe rugose virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI TaxID=158463;
RN [1]__TaxID=158463;
RP SEQUENCE FROM N.A.
RC STRAIN=Minas Gerais;
RA Rezende W.L., Goulart L.R., Parreira K.S., Figueiredo J.E.F.;
RT "The full-length DNA-A nucleotide sequence of a novel tomato-infecting
RT begomovirus, Tomato severe rugose virus, in Brazil."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029750; RAKS0357.1; -
DR InterPro; IPR001191; Geminiviridae.
DR Pfam; PF00799; Geminiviridae.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Geminiviridae.
SQ SEQUENCE 351 AA; 40122 MW; 87F937A4F873B6CF CRC64;

Query Match 83.0%; Score 298; DB 12; Length 351;
Best Local Similarity 80.0%; Pred. No. 1.4e-26;
Matches 56; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY	1	TLVWGEFQDGRSARGGQCTNSDAEALNSKKEALQIREKIPAAALFOFHNLNSL 60
Db	111	TLVWGEFQDGRSARGGQCTNSDAEALNSKKEALQIREKIPAAALFOFHNLNSL 170
QY	61	DRIFDKTPEP 70
Db	171	DRIFDKTPEP 180

```
RESULT 2
ID Q9E000 PRELIMINARY; PRT; 352 AA.
AC Q9E000;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Replication-associated protein.
GN AC1.
OS Tomato rugose mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=134599;
RN [1]
RA Fernandes J.J., Fontes E.P.B., Brommonschenkel S.H., Carvalho M.G.,
  Zambolim E.M., Zerbini F.M.;
  "Molecular Cloning and Characterization of Tomato rugose mosaic virus
  (TRMV), a Begomovirus Isolated from Tomatoes at Triangulo Mineiro,
  Minas Gerais, Brazil.";
  Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF291705; AAG15546.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR PRODOM; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 352 AA; 40012 MW; 47CD55838E24D613 CRC64;
Query Match 82.5%; Score 296; DB 12; Length 352;
Best Local Similarity 80.0%; Pred. No. 2.4e-26;
Matches 56; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
Qy 1 TLVWGFQVDRSARGGCGTNDAAAEALNASSKEALQIREKIPAAALFQFHNLSNL 60
Db 111 TLVWGFQVDRSARGGCGTNDAAAEALNASSKEALQIREKIPAAALFQFHNLSNL 170
Qy 61 DRIFDKTPEP 70
Db 171 DRIFAKAPEP 180
Query Match 79.9%; Score 287; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 1.6e-25;
Matches 54; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
Qy 1 TLVWGFQVDRSARGGCGTNDAAAEALNASSKEALQIREKIPAAALFQFHNLSNL 60
Db 111 TLVWGFQVDRSARGGCGTNDAAAEALNASSKEALQIREKIPAAALFQFHNLSNL 170
Qy 61 DRIFDKTPEP 70
Db 171 DRIFAKAPEP 180
RESULT 5
ID Q67574 PRELIMINARY; PRT; 361 AA.
AC Q67574;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative replicative protein.
GN AL1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
  Maxwell D.P., Russell D.R.;
  "Cloning of the complete DNA genomes of four bean-infecting
  geminiviruses and determining their infectivity by electric discharge
  particle acceleration.";
  Phytopathology 81:980-985 (1991).
RN [2]
SQ SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
  Morales F.J., Maxwell D.P.;
  "Differentiation of bean-infecting geminiviruses by nucleic acid
```

```

RT hybridization probes and aspects of bean golden mosaic in Brazil.";
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus.";
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M88686; AAA46312.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 77.2%; Score 277; DB 12; Length 361;
Best Local Similarity 77.6%; Pred. No. 4.2e-24;
Matches 52; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 WGEFQVDGRSARGGCTSNDAAEALNASSKEKALQIIREKIPAAALFQPHNLSNLDRI 63
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 WGHFQVDGRSARGGCTSNDAAEALNASSKEKALQIIREKIPAAALFQPHNLSNLDRI 172

QY 64 FDKTPEP 70
Db |||||
173 FTKAPDP 179

RESULT 6
Q9QDB1 PRELIMINARY; PRT; 225 AA.
ID Q9QDB1
AC Q9QDB1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Replication associated protein (Fragment).
GN REP.
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGMV-BR;
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RT Brazil.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF188708; AAF06318.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 225
SQ SEQUENCE 225 AA; 25766 MW; 1089CB6BD8D15B5D CRC64;

Query Match 76.8%; Score 275; DB 12; Length 225;
Best Local Similarity 77.6%; Pred. No. 4.1e-24;
Matches 52; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 4 WGEFQVDGRSARGGCTSNDAAEALNASSKEKALQIIREKIPAAALFQPHNLSNLDRI 63
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 WGHFQVDGRSARGGCTSNDAAEALNASSKEKALQIIREKIPAAALFQPHNLSNLDRI 172

QY 64 FDKTPEP 70
Db |||||
173 FKKPPEP 179

RESULT 7
O09727 PRELIMINARY; PRT; 226 AA.
ID O09727
AC O09727;

```

```

DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN REP.
OS Leonurus mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=58177;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lemv- Brazil 1;
RA Faria J.C., Maxwell D.P.;
RT "Variability in geminivirus associated with Phaseolus vulgaris in
RT Brazil.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U92532; AAB51157.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 226
SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;

Query Match 76.6%; Score 275; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 4.1e-24;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGRSARGGCTSNDAAEALNASSKEKALQIIREKIPAAALFQPHNLSN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
111 TVWGEFQVDGRSARGGCTSNDAAEALNASSKEKALQIIREKIPAAALFQPHNLSN 170

QY 61 DRIFDKTPEP 70
Db |||||
171 DRIFAKAPEP 180

RESULT 8
Q98693 PRELIMINARY; PRT; 185 AA.
ID Q98693
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Jamaica;
RA Roye M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed
RT species Sida spp, Macroptilium lathyroides, and Wissadula amplissima
RT from Jamaica.";
RL Plant Dis. 81:1251-1258(1997).
DR EMBL; U67926; AAB37865.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 185
SQ SEQUENCE 185 AA; 20975 MW; 3913850A025A5EE1 CRC64;

Query Match 75.5%; Score 271; DB 12; Length 185;
Best Local Similarity 71.4%; Pred. No. 9.6e-24;
Matches 50; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGRSARGGCTSNDAAEALNASSKEKALQIIREKIPAAALFQPHNLSN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
89 TVWGEFQVDGRSARGGCTSNDAAEALNASSKEKALQIIREKIPAAALFQPHNLSN 148

```



```

QY 61 DRIPDKTPEP 70
Db 149 DRIFSKPPEP 158

RESULT 9
Q9ELT8 PRELIMINARY; PRT; 314 AA.
AC Q9ELT8,
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Replication association protein.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RL Plant Dis. 82:1253-1257 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF298227; AAG01006.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 75.5%; Score 271; DB 12; Length 314;
Best Local Similarity 79.4%; Pred. No. 1.8e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 60
Db 110 TITWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 169

QY 61 DRIPDKTPEP 68
Db 170 DRIFSPPP 177

RESULT 10
Q9QSS5 PRELIMINARY; PRT; 364 AA.
AC Q9QSS5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RL States.";
RL Plant Dis. 82:1253-1257 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RL virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0 (1999).
DR EMBL; AF104036; AAD47173.1; -.
DR InterPro; IPR001191; Gemini_AL1.

Query Match 75.5%; Score 271; DB 12; Length 314;
Best Local Similarity 79.4%; Pred. No. 1.8e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 60
Db 110 TITWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 169

QY 61 DRIPDKTPEP 68
Db 170 DRIFSPPP 177

RESULT 11
Q8QPU4 PRELIMINARY; PRT; 235 AA.
AC Q8QPU4;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RA Ribeiro S.G., Ambrozovicus L.P., de Avila A.C., Calegario R.F.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049208; AAL82833.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 235 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BB0DD9C810 CRC64;

Query Match 74.7%; Score 268; DB 12; Length 235;
Best Local Similarity 74.6%; Pred. No. 2.9e-23;
Matches 50; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 4 WGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 63
Db 113 WGIQFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 172

QY 64 FDKTPEP 70
Db 173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

```

```

RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126611; AAM95995.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 208
SQ SEQUENCE 208 AA; 23667 MW; 51211D58FAD690A6 CRC64;

Query Match 74.4%; Score 267; DB 12; Length 208;
Best Local Similarity 71.4%; Pred. No. 3.2e-23;
Matches 50; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEALQIIREKIPAAALFOFHNLSNL 60
Db 110 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEAMKIIKEKLPKFLFOYHNSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 DRIFWKAQKP 179

RESULT 13
Q8JLY5 PRELIMINARY; PRT; 289 AA.
AC Q8JLY5;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;
RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126610; AAM95993.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 289
SQ SEQUENCE 289 AA; 32971 MW; 4ECF52F4C69C6764 CRC64;

Query Match 74.4%; Score 267; DB 12; Length 289;
Best Local Similarity 71.4%; Pred. No. 4.8e-23;
Matches 50; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEALQIIREKIPAAALFOFHNLSNL 60
Db 110 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEAMKIIKEKLPKFLFOYHNSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 DRIFWKAQKP 179

RESULT 14
P88975 PRELIMINARY; PRT; 149 AA.
AC P88975;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Macropitium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Jamaican;
RA Roye M.E.;
RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
DR EMBL; U75278; AAB36919.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 149
SQ SEQUENCE 149 AA; 16785 MW; E4CF5ED4C9CD508 CRC64;

Query Match 73.5%; Score 264; DB 12; Length 149;
Best Local Similarity 70.0%; Pred. No. 4.9e-23;
Matches 49; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEALQIIREKIPAAALFOFHNLSNL 60
Db 52 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEAMRIYKEKLPKFLFOYHNSNL 111

Qy 61 DRIFDKTPEP 70
Db 112 DRIFWKAQKP 121

RESULT 15
Q9Z089 PRELIMINARY; PRT; 190 AA.
ID Q9Z089
AC Q9Z089;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Tobacco leaf curl virus C1 and C4 genes, clone YOKOHAMA3-1, partial
DE and complete cds (Fragment).
GN C1.
OS Tobacco leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=67762;
RN [1]
RP SEQUENCE FROM N.A.
RA Ooi K., Ohshita S., Ishii I., Yahara T.;
RT "Molecular phylogeny of geminivirus infecting wild plants in Japan.";
RL J. Plant Res. 110:247-257(1997).
DR EMBL; AB001315; BAA34033.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 190
SQ SEQUENCE 190 AA; 21432 MW; AAC093D1D1610FAD CRC64;

Query Match 73.5%; Score 264; DB 12; Length 190;
Best Local Similarity 62.4%; Pred. No. 6.5e-23;
Matches 53; Conservative 6; Mismatches 10; Indels 16; Gaps 1;

Qy 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEALQIIREKIPAAALFOFHNLSNL 60
Db 85 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEALAIKEKLPKFLFOYHNSNL 144

Qy 61 DRI-----FKTPE 69
Db 145 DRIFAPLEVFCVPTASSFDQVPE 169

Search completed: December 23, 2003, 09:03:35
Job time : 25.3333 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds
(without alignments)
340.128 Million cell updates/sec

Title: US-09-289-346B-6
Perfect score: 357
Sequence: 1 TLVGEFQVDSRSGGQCT.....FAFALNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 15872573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1_ Geneseq 19Jun03.*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	357	100.0	70	21	AA18682
2	340	95.2	70	21	AA18677
3	340	95.2	356	21	AA18687
4	332	93.0	70	21	AA18685
5	329	92.2	70	21	AA18688
6	328	91.9	70	21	AA18692
7	326	91.3	70	21	AA18684
8	326	91.3	70	21	AA18690
9	325	91.0	70	21	AA18678

10	325	91.0	70	21	AA18686	Mutant peptide der
11	324	90.8	70	21	AA18689	Mutant peptide der
12	322	90.2	70	21	AA18680	Mutant peptide der
13	322	90.2	70	21	AA18691	Mutant peptide der
14	319	89.4	70	21	AA18681	Mutant peptide der
15	318	89.1	70	21	AA18683	Mutant peptide der
16	308	86.3	70	21	AA18679	Mutant peptide der
17	210	58.8	359	17	AA186870	Sardinian tomato y
18	210	58.8	359	17	AA186871	Sardinian tomato y
19	210	58.8	359	17	AA186872	Sardinian tomato y
20	206	57.7	353	18	AA186873	Bean golden mosaic
21	206	57.7	353	18	AA186874	Bean golden mosaic
22	206	57.7	353	18	AA186875	Bean golden mosaic
23	206	57.7	353	18	AA186876	Bean golden mosaic
24	206	57.7	353	18	AA186877	Bean golden mosaic
25	204	57.1	353	18	AA186878	ORF 4 gene product
26	204	57.1	361	18	AA186879	Tomato mottle viru
27	204	57.1	361	18	AA186880	Tomato mottle viru
28	204	57.1	361	18	AA186881	Tomato mottle viru
29	204	57.1	361	18	AA186882	Tomato mottle viru
30	199.5	55.9	50	23	AA186883	Retinoblastoma-bin
31	197.5	55.3	361	8	AA186884	Product of ORF 4 f
32	192	53.8	362	19	AA186885	Tobacco leaf curl
33	191	53.5	357	18	AA186886	Tomato yellow leaf
34	191	53.5	357	18	AA186887	Tomato yellow leaf
35	191	53.5	357	18	AA186888	Tomato yellow leaf
36	183	51.3	357	18	AA186889	Tomato yellow leaf
37	104	29.1	142	24	AA186890	Tomato yellow leaf
38	76.5	21.4	665	22	AA186891	Drosophila melanog
39	76	21.3	857	23	AA186892	Protein fragment #
40	67	18.8	447	21	AA186893	Human GTPase assoc
41	67	18.8	447	21	AA186894	Human secreted pro
42	67	18.8	447	21	AA186895	Membrane-bound pro
43	67	18.8	447	21	AA186896	Human adult aorta
44	67	18.8	447	22	AA186897	Human PRO polypept
45	67	18.8	447	22	AA186898	Human polypeptide,

ALIGNMENTS

RESULT 1
AA18682
ID AA18682 standard; peptide; 70 AA.

XX AA18682;

XX 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (All) protein.

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

KW ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 52

FT /note= "wild type residue replaced with Ala"

FT Misc-difference 54

FT /note= "wild type residue replaced with Ala"

FT Misc-difference 55

FT /note= "wild type residue replaced with Ala"

XX WO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346.

```

XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT
XX PS Claim 53; Page 44-45; 73pp; English.
XX CC
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
XX Query Match 100.0%; Score 357; DB 21; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-37;
XX Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60
Db 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
XX
XX RESULT 2
XX AAB18677
XX ID AAB18677 standard; peptide; 70 AA.
XX AC AAB18677;
XX XX
XX XX Peptide fragment from Rep protein of TGMV (amino acids 110-179).
XX DT 22-JAN-2001 (first entry)
XX DE
XX DE
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS
XX OS Tomato golden mosaic virus.
XX PN WO200054573-A1.
XX XX
XX XX 21-SEP-2000.
XX XX
XX XX 15-MAR-2000; 2000WO-US06759.
XX PF
XX PF 18-MAR-1999; 99US-0125004.
XX PR
XX PR 09-APR-1999; 99US-0289346.
XX XX
XX XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX PA
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX PI WPI; 2000-618851/59.
XX DR
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT
XX PS Disclosure; Page 18; 73pp; English.
XX CC
XX CC The present sequence is derived from a geminivirus replication (Rep)
XX CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
XX CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
XX CC with other viral and host proteins. Mutants of the AL1 protein are used
XX CC to produce transgenic plants. The mutation in AL1 is present in a
XX CC ribosome binding region, and expression of mutant AL1 protein imparts
XX CC increased resistance to geminivirus infection in the plant. Mutant AL1
XX CC proteins are useful for producing plants having increased resistance or
XX CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
XX CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
XX CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
XX CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
XX CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
XX CC beet curly top virus.
XX SQ Sequence 70 AA;
XX Query Match 95.2%; Score 340; DB 21; Length 70;
XX Best Local Similarity 95.7%; Pred. No. 1.8e-35;
XX Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60
Db 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
XX
XX RESULT 3
XX AAB18687
XX ID AAB18687 standard; peptide; 356 AA.
XX AC AAB18687;
XX XX
XX XX 22-JAN-2001 (first entry)
XX DT
XX DE
XX DE Amino acid sequence of a geminivirus replication protein of TGMV.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS
XX OS Tomato golden mosaic virus.
XX FH Key Location/Qualifiers
XX FT Misc-difference 354 /note= "unspecified amino acid"
XX FT
XX PN WO200054573-A1.
XX XX
XX XX 21-SEP-2000.
XX XX
XX XX 15-MAR-2000; 2000WO-US06759.
XX PF
XX PF 18-MAR-1999; 99US-0125004.
XX PR
XX PR 09-APR-1999; 99US-0289346.
XX XX
XX XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX PA
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX PI WPI; 2000-618851/59.
XX DR
XX DR Transgenic plants with increased resistance to geminivirus infection
XX PT

```

comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant ALI protein with a mutation in the Rb Binding region

- Disclosure; Page 47-48; 73pp; English.

The present sequence represents a geminivirus replication (Rep) protein, which is also known as ALI. ALI binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the ALI protein are used to produce transgenic plants. The mutation in ALI is present in a ribosome binding region, and expression of mutant ALI protein imparts increased resistance to geminivirus infection in the plant. Mutant ALI proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

XX XX Sequence 356 AA;

Query Match 95.2%; Score 340; DB 21; Length 356;
Best Local Similarity 95.7%; Pred. No. 1.4e-34;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSGRGCGQTSDAAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 110 TLVWGEFQVDRSGRGCGQTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSL 169
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 DRIFDKTPEP 70
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 170 DRIFDKTPEP 179

RESULT 4
AAB18685
ID AAB18685 standard; peptide; 70 AA.
XX AAB18685;
AC AAB18685;
XX AAB18685;
DT 22-JAN-2001 (first entry)
DE Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.
XX Geminivirus; replication protein; Rep protein; ALI; transgenic plant;
KW ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
OS Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 10 /note= "wild type residue replaced with Ala"
FT
FW WO200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
PA
XX Hanley-Bowdoin L, Orozco BM, Kong L;
PI WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence

PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX
 XX Disclosure; Page 48; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;

Query Match 92.2%; Score 329; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 4.6e-34;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEALQIREKIPKYLFAFALNSNL 60
 DB 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEALQIREKIPKYLQFHNLSNL 60
 QY 61 DRFDKTPPEP 70
 DB 61 DRFDKTPPEP 70

RESULT 6
 AAB18692
 ID AAB18692 standard; peptide; 70 AA.
 AC AAB18692;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 XX Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 FH FT Misc-difference 66 /note= "wild type residue replaced with Ala"
 FT FT Misc-difference 69 /note= "wild type residue replaced with Ala"
 FT FT
 XX WO200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX

PT Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX
 XX Disclosure; Page 50; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;

Query Match 91.9%; Score 328; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 6.1e-34;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEALQIREKIPKYLFAFALNSNL 60
 DB 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEALQIREKIPKYLQFHNLSNL 60
 QY 61 DRFDKTPPEP 70
 DB 61 DRFDATPAP 70

RESULT 7
 AAB18684
 ID AAB18684 standard; peptide; 70 AA.
 AC AAB18684;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 XX Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 FH FT Misc-difference 7 /note= "wild type residue replaced with Ala"
 FT FT Misc-difference 8 /note= "wild type residue replaced with Ala"
 FT FT
 XX WO200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX
 XX Claim 52; Page 45; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;

Query Match 91.3%; Score 326; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 1.1e-33;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGQTSNDAAAEALNASSKEALQIIREKIPEKYLPAALNSNL 60
 DB 1 TLVWGEAAVDGSRAGGCGQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLNSNL 60

QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70

RESULT 8

AAB18690
 ID AAB18690 standard; peptide; 70 AA.

AC AAB18690;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.

OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 27 /note= "wild type residue replaced with Ala"

FT Misc-difference 30 /note= "wild type residue replaced with Ala"

XX WO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX

DR WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -

XX Disclosure; Page 49; 73pp; English.

CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.

SQ Sequence 70 AA;

Query Match 91.3%; Score 326; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 1.1e-33;

Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGQTSNDAAAEALNASSKEALQIIREKIPEKYLPAALNSNL 60

DB 1 TLVWGEFQVDRSARGGCGQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLNSNL 60

QY 61 DRIFDKTPEP 70

DB 61 DRIFDKTPEP 70

RESULT 9

AAB18678

ID AAB18678 standard; peptide; 70 AA.

AC AAB18678;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 12 /note= "wild type residue replaced with Ala"

FT Misc-difference 13 /note= "wild type residue replaced with Ala"

FT Misc-difference 15 /note= "wild type residue replaced with Ala"

XX WO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

```

XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
XX Claim 53; Page 42-43; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 91.0%; Score 325; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.5e-33;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 TLVWGEFQVDRSGAGCGCOTSDAAALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60
Db 1 TLVWGEFQVDRSGAGCGCOTSDAAALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 10
AAB18686
ID AAB18686 standard; peptide; 70 AA.
XX
XX AAB18686;
XX
DT 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX OS Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 24 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 25 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 26 /note= "wild type residue replaced with Leu"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX

```

```

PR
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
XX Claim 53; Page 46; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 91.0%; Score 325; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.5e-33;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 TLVWGEFQVDRSGAGCGCOTSDAAALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60
Db 1 TLVWGEFQVDRSGAGCGCOTSDAAALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 11
AAB18689
ID AAB18689 standard; peptide; 70 AA.
XX
XX AAB18689;
XX
DT 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX OS Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 22 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX

```



```

PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection.
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant ALI protein with a mutation in the Rb binding region
XX
XX Disclosure; Page 48-49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 90.8%; Score 324; DB 21; Length 70;
XX Best Local Similarity 92.9%; Pred. No. 2e-33;
XX Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 1 TLVWGEFQVDRSARGGCCTSDNDAAEALNASSKEALQIIREKIPKYLFAFALNSNL 60
DB 1 TLVWGEFQVDRSARGGCCTSDNDAAEALNASSKEALQIIREKIPKYLFAFALNSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
XX
RESULT 12
AAB18680
ID AAB18680 standard; peptide; 70 AA.
XX
XX AAB18680;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 42 /note= "wild type residue replaced with Ala"
XX
XX Misc-difference 43 /note= "wild type residue replaced with Ala"
XX
XX Misc-difference 44 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant ALI protein with a mutation in the Rb binding region
XX
XX Claim 52; Page 43-44; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 90.2%; Score 322; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 3.5e-33;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
QY 1 TLVWGEFQVDRSARGGCCTSDNDAAEALNASSKEALQIIREKIPKYLFAFALNSNL 60
DB 1 TLVWGEFQVDRSARGGCCTSDNDAAEALNASSKEALQIIREKIPKYLFAFALNSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
XX
RESULT 13
AAB18691
ID AAB18691 standard; peptide; 70 AA.
XX
XX AAB18691;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 34 /note= "wild type residue replaced with Ala"
XX
XX Misc-difference 35 /note= "wild type residue replaced with Ala"
XX
XX Misc-difference 36 /note= "wild type residue replaced with Ala"
XX
XX

```


FT Misc-difference 61 /note= "wild type residue replaced with Ala"
FT /note= "wild type residue replaced with Ala"
FT Misc-difference 62
FT /note= "wild type residue replaced with Ala"
XX

FN WO200054573-Al.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346.

XX (UYN-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

DR Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant Al1 protein with a mutation in the Rb binding region
XX

XX Claim 53; Page 45; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as Al1. Al1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the Al1
XX protein are used to produce transgenic plants. The mutation in Al1 is
XX present in a ribosome binding region, and expression of mutant Al1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant Al1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;

Query Match 89.1%; Score 318; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.1e-32;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDCRSARGGCGTSDNDAAEALNASSKEEALQIREKIPEKYLFAFALNSNL 60

Db 1 TLVWGEFQVDCRSARGGCGTSDNDAAEALNASSKEEALQIREKIPEKYLFOFHNLSAL 60

Qy 61 DRIFDKTPEP 70

Db 61 AAIFDKTPEP 70

Search completed: December 23, 2003, 08:56:30
Job time : 32.6667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 11.6667 Seconds
(without alignments)
253.865 Million cell updates/sec

Title: US-09-289-346B-6
Perfect score: 357
Sequence: 1 TLVWGEFQVGRSARGCQT.....FAFAALNSLDRIFDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCUTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	210	58.8	359	3	US-08-809-103B-2 Sequence 2, Appli
2	210	58.8	359	3	US-08-809-103B-4 Sequence 4, Appli
3	210	58.8	359	3	US-08-809-103B-6 Sequence 6, Appli
4	210	58.8	359	3	US-08-809-103B-8 Sequence 8, Appli
5	206	57.7	353	3	US-08-838-151A-44 Sequence 44, Appli
6	206	57.7	353	3	US-08-838-151A-46 Sequence 46, Appli
7	206	57.7	353	3	US-08-838-151A-49 Sequence 49, Appli
8	206	57.7	353	3	US-08-838-151A-52 Sequence 52, Appli
9	206	57.7	353	3	US-08-838-151A-55 Sequence 55, Appli
10	204	57.1	361	3	US-08-838-151A-2 Sequence 2, Appli
11	204	57.1	361	3	US-08-838-151A-4 Sequence 4, Appli
12	204	57.1	361	3	US-08-838-151A-6 Sequence 6, Appli
13	204	57.1	361	3	US-08-838-151A-8 Sequence 8, Appli
14	191	53.5	357	3	US-08-838-151A-24 Sequence 24, Appli
15	191	53.5	357	3	US-08-838-151A-27 Sequence 27, Appli
16	191	53.5	357	3	US-08-838-151A-30 Sequence 30, Appli
17	183	51.3	357	3	US-08-838-151A-20 Sequence 20, Appli
18	67	18.8	447	4	US-09-996-243-369 Sequence 369, App
19	67	18.8	447	4	US-09-482-273-128 Sequence 128, App
20	67	18.8	456	4	US-09-482-273-229 Sequence 229, App
21	64.5	18.1	1713	3	US-08-600-982-24 Sequence 24, Appli
22	64.5	18.1	1713	3	PCT-US94-10261A-24 Sequence 24, Appli
23	63.5	17.8	2161	1	US-07-745-206A-2 Sequence 2, Appli
24	63.5	17.8	2161	1	US-08-455-543A-49 Sequence 49, Appli
25	63.5	17.8	2161	1	US-08-455-543A-51 Sequence 51, Appli
26	63.5	17.8	2161	2	US-08-223-305C-49 Sequence 49, Appli
27	63.5	17.8	2161	2	US-08-223-305C-51 Sequence 51, Appli

28	63.5	17.8	2161	2	US-08-311-363-2 Sequence 2, Appli
29	63	17.6	293	4	US-09-414-276-3 Sequence 3, Appli
30	63	17.6	335	4	US-09-414-276-6 Sequence 6, Appli
31	60.5	16.9	131	3	US-08-838-151A-14 Sequence 14, Appli
32	60.5	16.9	244	4	US-09-328-352-4541 Sequence 4541, Ap
33	60	16.8	531	4	US-08-976-063B-34 Sequence 34, Appli
34	58.5	16.4	1203	4	US-09-351-200-2 Sequence 2, Appli
35	58	16.2	173	4	US-09-266-225D-2 Sequence 2, Appli
36	58	16.2	446	3	US-08-672-814D-11 Sequence 11, Appli
37	58	16.2	446	3	US-09-333-696-11 Sequence 11, Appli
38	58	16.2	446	4	US-09-282-218A-19 Sequence 19, Appli
39	55.5	15.5	426	4	US-09-252-991A-20262 Sequence 20262, A
40	55.5	15.5	593	3	US-09-234-393-54 Sequence 54, Appli
41	55.5	15.5	593	4	US-09-865-171-54 Sequence 54, Appli
42	55	15.4	288	4	US-09-328-352-6485 Sequence 6485, Ap
43	55	15.4	374	3	US-09-091-405-2 Sequence 2, Appli
44	55	15.4	498	2	US-08-511-485-13 Sequence 13, Appli
45	55	15.4	498	4	US-09-201-936-13 Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-08-809-103B-2
; Sequence 2, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GROENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: US894AL CNR TOM
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-2

Query Match 58.8%; Score 210; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 4.8e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

```
QY      2 LVWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNLD 61
DB      111 LEWGTFTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170
QY      62 RIFDKTPEP 70
DB      171 KVFQVPPAP 179

RESULT 2
US-08-809-103B-4
; Sequence 4, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: FR 94.11040
; APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-4

Query Match      58.8%; Score 210; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 4.8e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY      2 LVWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNLD 61
DB      111 LEWGTFTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170
QY      62 RIFDKTPEP 70
DB      171 KVFQVPPAP 179

RESULT 3
US-08-809-103B-6
; Sequence 6, Application US/08809103B
```

```
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: FR 94.11040
; APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-6

Query Match      58.8%; Score 210; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 4.8e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY      2 LVWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNLD 61
DB      111 LEWGTFTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170
QY      62 RIFDKTPEP 70
DB      171 KVFQVPPAP 179

RESULT 4
US-08-809-103B-8
; Sequence 8, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/809,103B
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8

Query Match 58.8%; Score 210; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 4.8e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGFEQVDGSRARGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLPFAALNSMLD 61
Db 111 LEWGTFFQIDGSRARGGCGQTANDAYAKAINAGSKSQALDVKEIAPRDYVLHFHNSMLD 170

Qy 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 5
US-08-838-151A-44
; Sequence 44, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

Query Match 57.7%; Score 206; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.6e-19;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-44

Query Match 57.7%; Score 206; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.6e-19;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLWGFEQVDGSRARGGCGTSDNAAAEALNASSKEEALQIIREKIPEKYLPFAALNSNL 60
Db 110 TIWGFQFQVDGSRARGGCGQSANDSYAKALNADSIESTILKBEQPKDYVLQHNIRSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 6
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

Query Match 57.7%; Score 206; DB 3; Length 353;
```

```
; Best Local Similarity 57.1%; Pred. No. 1.6e-19;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGSCGTSNDAAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TIEWGQFQVDSARGSCGTSNDAAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 7
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; APPLICATION NUMBER: US-08-838-151A-49

Query Match 57.7%; Score 206; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.6e-19;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGSCGTSNDAAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TIEWGQFQVDSARGSCGTSNDAAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 8
US-08-838-151A-52
; Sequence 52, Application US/08838151A
; Patent No. 6291743
```

```
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; APPLICATION NUMBER: US-08-838-151A-52

Query Match 57.7%; Score 206; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.6e-19;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGSCGTSNDAAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TIEWGQFQVDSARGSCGTSNDAAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 9
US-08-838-151A-55
; Sequence 55, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
```

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-2

Query Match 57.1%; Score 204; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.1e-19;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0

QY 1 TLVWGEFQVDRSARGGCQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 60
DB 110 TIWGDFOIDGRSARGGQSSANDSYAKALNASSVQSALAVLREEQPKDFVLQHNIRSNL 169

QY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 11
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-4

Query Match 57.1%; Score 204; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.1e-19;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0

QY 1 TLVWGEFQVDRSARGGCQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 60
DB 110 TIWGDFOIDGRSARGGQSSANDSYAKALNASSVQSALAVLREEQPKDFVLQHNIRSNL 169

QY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 10
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460

```

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-2

Query Match 57.1%; Score 204; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.1e-19;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0

QY 1 TLVWGEFQVDRSGRGCGCQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 60
DB 110 TIWGDFOIDGRSARGGQSQSANDSYAKALNASSVQSALAVLREEQPKDFVLQHNIRSNL 169

QY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 11
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-4

Query Match 57.1%; Score 204; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.1e-19;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0

QY 1 TLVWGEFQVDRSGRGCGCQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 60
DB 110 TIWGDFOIDGRSARGGQSQSANDSYAKALNASSVQSALAVLREEQPKDFVLQHNIRSNL 169

QY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179

US-08-838-151A-55
Query Match 57.7%; Score 206; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.6e-19;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGCQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 60
DB 110 TIWGDFOIDGRSARGGQSQSANDSYAKALNADSIESTILKEQPKDYVLQHNIRSNL 169

QY 61 DRIFDKTPEP 70
DB 170 ERIFVKVPEP 179

RESULT 10
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460

```



```

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 12
US-08-838-151A-6
; Sequence 6, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6

Query Match 57.1%; Score 204; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.1e-19;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
Db 110 TIWGDGFQIDGRSARGGCGQSANDSYAKALNASSVQSALAVUREEQPKDFVLQNHINRSL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 14
US-08-838-151A-24
; Sequence 24, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6

Query Match 57.1%; Score 204; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.1e-19;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
Db 110 TIWGDGFQIDGRSARGGCGQSANDSYAKALNASSVQSALAVUREEQPKDFVLQNHINRSL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 13
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6

Query Match 57.1%; Score 204; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.1e-19;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
Db 110 TIWGDGFQIDGRSARGGCGQSANDSYAKALNASSVQSALAVUREEQPKDFVLQNHINRSL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

```

```

; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-838-151A-24

Query Match 53.5%; Score 191; DB 3; Length 357;
Best Local Similarity 62.3%; Pred. No. 1.7e-17;
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 4 WGFQVDGRGARGCGQTSNDAAEALNASKEEALQIIRKIKYLFAPALNSNLDRI 63
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 111 FGVSQIDGRGARGGQSQSANDAYAEALNSGSKSEALNIIKEKAPKDYILQFHNLSSNLDRI 170

Qy 64 F 64
|
Db 171 F 171

```

RESULT 15
 US-08-838-151A-27
 Sequence 27, Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Luu, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 TITLE OF INVENTION: Genes
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-27

```

Query Match          53.5%; Score 191; DB 3; Length 357;
Best Local Similarity 62.3%; Pred. No. 1.7e-17;
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY      4   WGEFVDGRSARGGCOTSNDAAEALNAGSKKEALQIIREKIPKYLFAFAALNSNLDR I 63
        :|:|||||||:|||||||:|||||||:|||||||:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      111 FGVSQIDGRSARGGQQSQANDAYEALNAGSKSEALNILKENAPDYILOPHNLSSNLDR I 170

QY      64 F 64
       |
Db     171 F 171

Search completed: December 23, 2003, 08:59:34
Job time : 11.6667 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds
(without alignments)
172.015 Million cell updates/sec

Title: US-09-289-346B-6
Perfect score: 357
Sequence: 1 TLVWGFQVDSARGGCQT.....FAFALNSLDRIFDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	357	100.0	70	10	US-09-289-346A-6
2	340	95.2	70	10	US-09-289-346A-1
3	340	95.2	356	10	US-09-289-346A-11
4	332	93.0	70	10	US-09-289-346A-9
5	329	92.2	70	10	US-09-289-346A-12
6	328	91.9	70	10	US-09-289-346A-16
7	326	91.3	70	10	US-09-289-346A-8
8	326	91.3	70	10	US-09-289-346A-14
9	325	91.0	70	10	US-09-289-346A-2
10	325	91.0	70	10	US-09-289-346A-10
11	324	90.8	70	10	US-09-289-346A-13
12	322	90.2	70	10	US-09-289-346A-4
13	322	90.2	70	10	US-09-289-346A-15
14	319	89.4	70	10	US-09-289-346A-5
15	318	89.1	70	10	US-09-289-346A-7

16	308	86.3	70	10	US-09-289-346A-3
17	67	18.8	447	9	US-09-989-722-369
18	67	18.8	447	9	US-09-989-723-369
19	67	18.8	447	9	US-09-989-279-369
20	67	18.8	447	9	US-09-989-727-369
21	67	18.8	447	10	US-09-989-731-369
22	67	18.8	447	10	US-09-989-732-369
23	67	18.8	447	10	US-09-991-073-369
24	67	18.8	447	10	US-09-990-442-369
25	67	18.8	447	10	US-09-991-163-369
26	67	18.8	447	10	US-09-993-604-369
27	67	18.8	447	10	US-09-990-456-369
28	67	18.8	447	10	US-09-989-721-369
29	67	18.8	447	10	US-09-992-598-369
30	67	18.8	447	10	US-09-989-293A-369
31	67	18.8	447	10	US-09-989-735-369
32	67	18.8	447	10	US-09-990-444-369
33	67	18.8	447	10	US-09-991-181-369
34	67	18.8	447	10	US-09-989-730-369
35	67	18.8	447	10	US-09-990-436-369
36	67	18.8	447	10	US-09-993-687-369
37	67	18.8	447	11	US-09-989-734-369
38	67	18.8	447	11	US-09-997-653-369
39	67	18.8	447	11	US-09-993-667-369
40	67	18.8	447	11	US-09-997-428-369
41	67	18.8	447	11	US-09-997-666-369
42	67	18.8	447	11	US-09-990-438-369
43	67	18.8	447	11	US-09-990-562-369
44	67	18.8	447	11	US-09-990-711-369
45	67	18.8	447	11	US-09-984-271-128

ALIGNMENTS

RESULT 1

US-09-289-346A-6
; Sequence 6, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-die
; APPLICANT: Grisseem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (52)..(55)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (QFHN165->AFAA165).
US-09-289-346A-6

Query Match	100.0%;	Score 357;	DB 10;	Length 70;
Best Local Similarity	100.0%;	Pred. No. 3.9e-39;		
Matches	70;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	TLVWGFQVDSARGGCQTSNDAAALNASSKEEALQIREKIPKYLFAFALNSNL	60	
Db	1	TLVWGFQVDSARGGCQTSNDAAALNASSKEEALQIREKIPKYLFAFALNSNL	60	
Qy	61	DRIFDKTPEP	70	

```
Db          110 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 169
QY          61 DRIFDKTPEP 70
          |||||
Db          170 DRIFDKTPEP 179

RESULT 4
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match          93.0%; Score 332; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 7.3e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY          1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
Db          1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
QY          61 DRIFDKTPEP 70
          |||||
Db          61 DRIFDKTPEP 70

RESULT 5
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12

Query Match          92.2%; Score 329; DB 10; Length 70;

Db          110 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 169
QY          61 DRIFDKTPEP 70
          |||||
Db          170 DRIFDKTPEP 179

RESULT 4
US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1

Query Match          95.2%; Score 340; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 6.5e-37;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
Db          1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
QY          61 DRIFDKTPEP 70
          |||||
Db          61 DRIFDKTPEP 70

RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match          95.2%; Score 340; DB 10; Length 356;
Best Local Similarity 95.7%; Pred. No. 5.7e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
          |||||
```

```
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AA118).
US-09-289-346A-8

Query Match          91.3%; Score 326; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 4.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||
Db 1 TLVWGFQVDGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 6
US-09-289-346A-16
; Sequence 16, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-16

Query Match          91.9%; Score 328; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||
Db 1 TLVWGFQVDGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 7
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
```

```
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AA118).
US-09-289-346A-8

Query Match          91.3%; Score 326; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 4.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||
Db 1 TLVWGFQVDGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 8
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match          91.3%; Score 326; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 4.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||
Db 1 TLVWGFQVDGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 9
US-09-289-346A-2
; Sequence 2, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
```

```
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAAA125).
US-09-289-346A-2

Query Match          91.0%; Score 325; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 6e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCOTSDNDAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
DB 1 TLVWGEFQVDRSARGGCOTSDNDAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAAL36->LLLL136).
US-09-289-346A-10

Query Match          91.0%; Score 325; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 6e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCOTSDNDAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
DB 1 TLVWGEFQVDRSARGGCOTSDNLLLEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (42)..(44)
; OTHER INFORMATION: Description of Artificial sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAAA154).
US-09-289-346A-4

Query Match          90.2%; Score 322; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.5e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCOTSDNDAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
DB 1 TLVWGEFQVDRSARGGCOTSDNDAAEALNASSKEEALQIIRKIPKYLFAFALNSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match      90.2%; Score 322; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.5e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60
Db      1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60

Qy      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

RESULT 14
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (EKY159->AAA159).
US-09-289-346A-5

Query Match      89.4%; Score 319; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 3.7e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60
Db      1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60

Qy      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

```

```

RESULT 15
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDRI72->ALAA172).
US-09-289-346A-7

Query Match      89.1%; Score 318; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 4.9e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60
Db      1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSAL 60

Qy      61 DRIFDKTPEP 70
Db      61 AAIFDKTPEP 70

Search completed: December 23, 2003, 09:43:30
Job time : 77 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds
(without alignments)
673.181 Million cell updates/sec

Title: US-09-289-346B-6
Perfect score: 357
Sequence: 1 TLVWGEFQVGRSARGGCQT.....FAFAALNSLDRIFDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340	95.2	352	1 QQCVL1	Al1 protein - toma
2	240	67.2	361	1 QQCVPF	Al1 protein - toma
3	227	63.6	358	2 S07594	hypothetical prote
4	220	61.6	362	1 JQ1887	Al1 protein - toma
5	217	60.8	359	2 S39211	gene Cl protein -
6	212	59.4	351	2 JQ2327	Al1 protein - Indi
7	210	58.8	359	2 S22593	hypothetical prote
8	209	58.5	349	2 JQ2300	replicase - pepper
9	209	58.5	349	2 S31875	Al1 protein - pepp
10	204	57.1	359	2 S39235	gene Cl protein -
11	203	56.9	355	1 QQCVM1	AV1 protein - abut
12	200	56.0	358	1 JQ1870	Al1 protein - toma
13	200	56.0	385	2 S28360	Al1 protein - beet
14	193	54.1	360	2 S59885	replication-associ
15	191	53.5	357	1 QQCVC1	Al1 protein - toma
16	118	33.1	131	2 S45059	AC1 protein (clone
17	104	29.1	347	1 QQCVS1	Al1 protein - squa
18	67	18.8	447	2 T12544	hypothetical prote
19	64.5	18.1	587	2 JCI419	Fc gamma (19G) rec
20	64.5	18.1	1713	2 A55347	adhesive ligand ep
21	63.5	17.8	180	2 D84082	hypothetical prote
22	63.5	17.8	1610	2 A46227	voltage-dependent
23	63.5	17.8	1646	2 JH0422	voltage-dependent
24	63.5	17.8	2161	2 JH0564	calcium channel al
25	63.5	17.8	2181	2 A38198	calcium channel al
26	63.5	17.8	2203	2 T42742	voltage-dependent
27	63	17.6	316	2 C82085	conserved hypothet
28	62.5	17.5	1033	2 E97700	hypothetical prote
29	62	17.4	338	2 AG3582	iron(III)-binding

probably O-sialogl
acetyl-CoA C-acety
probable large ATP
protein-Npi-phosph
YNT20 protein - ye
Cl protein - tobac
phytoene synthase
phytoene synthase
probable ferrichro
phage-related prot
zinc finger protei
probable peptidyl-
gamma-aminobutyrat
diaminobutyrate-py
hypothetical prote
hypothetical prote

ALIGNMENTS

RESULT 1

QCCVL1
Al1 protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994
C:Accession: A04170
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
A:Residues: 1-352 <HAM>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 95.2%; Score 340; DB 1; Length 352;
Best Local Similarity 95.7%; Pred. No. 4.5e-31;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGEFQVGRSARGGCQTNDAAAALNASSKEALQIIREKIPEKYLFAALNSNL 60
DB 111 TLVWGEFQVGRSARGGCQTNDAAAALNASSKEALQIIREKIPEKYLFOFHNLSNL 170
QY 61 DRIFDKTPEP 70
DB 171 DRIFDKTPEP 180

RESULT 2

QCCVPF
Al1 protein - potato yellow mosaic virus (isolate Venezuela)
C:Species: potato yellow mosaic virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C:Accession: JU0364
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel
A:Reference number: JU0362; MUID:91311403; PMID:1856690
A:Accession: JU0364
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-361 <COU>
C:Cross-references: GB:D00940; NID:g222458; PIDN:BAA00782.1; PID:g222459
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 67.2%; Score 240; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 1.2e-19;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGCQTNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60
DB 110 TLVWGEFQVDSARGCGCQTNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 169
QY 61 DRIFDKTPEP 69
DB 170 DRIFDKAPE 178

RESULT 3
S07594
hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)
C:Species: cassava latent virus
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C:Accession: S07594
R:Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
Nucleic Acids Res. 18, 197-198, 1990
A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A:Reference number: S07590; MUID:90174930; PMID:2308831
A:Accession: S07594
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <NOR>
A:Cross-references: EMBL:X17095; NID:g59371; PIDN:CAA34953.1; PID:g59376
C:Genetics:
A:Map position: segment DNAL
C:Superfamily: tomato golden mosaic virus All protein

Query Match 63.6%; Score 227; DB 2; Length 358;
Best Local Similarity 60.8%; Pred. No. 3.6e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGCQTNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60
DB 109 TVWGEFQVDSARGCGCQTNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 168
QY 61 DRIFDKTPEP 70
DB 169 DRIFQEPAP 178

RESULT 4
JQ1887
All protein - tomato yellow leaf curl virus (strain Australia)
N:Alternate names: CI protein
C:Species: tomato yellow leaf curl virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
C:Accession: JQ1887
R:Dy, I.B.; Rigden, J.E.; Krake, L.R.; Mullineaux, P.M.; Rezaian, M.A.
J. Gen. Virol. 74, 147-151, 1993
A:Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.
A:Reference number: JQ1885; MUID:93139778; PMID:8423446
A:Accession: JQ1887
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <DRY>
A:Cross-references: GB:S53251
C:Superfamily: tomato golden mosaic virus All protein

Query Match 61.6%; Score 220; DB 1; Length 362;
Best Local Similarity 52.9%; Pred. No. 2.3e-17;
Matches 45; Conservative 9; Mismatches 15; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDSARGCGCQTNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60
DB 110 TLVWGEFQVDSARGCGCQTNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 169
QY 61 DRI-----FDKTPPE 69

Query Match 59.4%; Score 212; DB 2; Length 351;
Best Local Similarity 62.7%; Pred. No. 1.8e-16;
Matches 42; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 4 WGEFQVDSARGCGCQTNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSLDRI 63
DB 113 WGTFTQIDGRSARGCGCQTNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSLDRI 172
QY 64 FDKTPEP 70
DB 173 FTKPPPP 179

RESULT 7
S22593
hypothetical protein C4 - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999
C:Accession: S22593
R:Kheyr-pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, E.
Nucleic Acids Res. 19, 6763-6769, 1991
A:Title: Tomato yellow leaf curl virus from Sardinia is a whitefly transmitted monopart
A:Reference number: S22588; MUID:92107660; PMID:1840676

DB 170 DRIFTPPLEVTVSPFLSSSFDRVPE 194

RESULT 5
S39211
Gene C1 protein - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C:Accession: S39211
R:Norris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.
submitted to the EMBL Data Library, August 1993
A:Description: High similarity among the tomato yellow leaf curl virus isolates from th
A:Reference number: S39209
A:Accession: S39211
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <NOR>
A:Cross-references: EMBL:Z25751; NID:g433655; PIDN:CAA81026.1; PID:g433658
C:Superfamily: tomato golden mosaic virus All protein

Query Match 60.8%; Score 217; DB 2; Length 359;
Best Local Similarity 59.4%; Pred. No. 5.1e-17;
Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDSARGCGCQTNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSLD 61
DB 111 LEWGTFTQIDGRSARGCGCQTNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSLD 170
QY 62 RIFDKTPEP 70
DB 171 RVFQVPPAP 179

RESULT 6
JQ2327
All protein - Indian cassava mosaic virus
N:Alternate names: replication-associated protein
C:Species: Indian cassava mosaic virus
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 20-Sep-1999
C:Accession: JQ2327; S35883
R:Hong, Y.G.; Robinson, D.J.; Harrison, B.D.
J. Gen. Virol. 74, 2437-2443, 1993
A:Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-tra
A:Reference number: JQ2326; MUID:94085670; PMID:8245859
A:Accession: JQ2327
A:Molecule type: DNA
A:Residues: 1-351 <HON>
A:Cross-references: EMBL:Z24758; NID:g395351; PIDN:CAA80891.1; PID:g584046
C:Superfamily: tomato golden mosaic virus All protein

Query Match 59.4%; Score 212; DB 2; Length 351;
Best Local Similarity 62.7%; Pred. No. 1.8e-16;
Matches 42; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 4 WGEFQVDSARGCGCQTNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSLDRI 63
DB 113 WGTFTQIDGRSARGCGCQTNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSLDRI 172
QY 64 FDKTPEP 70
DB 173 FTKPPPP 179

RESULT 7
S22593
hypothetical protein C4 - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999
C:Accession: S22593
R:Kheyr-pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, E.
Nucleic Acids Res. 19, 6763-6769, 1991
A:Title: Tomato yellow leaf curl virus from Sardinia is a whitefly transmitted monopart
A:Reference number: S22588; MUID:92107660; PMID:1840676

C:Species: tomato mottle virus
C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
C:Accession: JQ1870
R:Abouzid, A.M.; Polston, J.E.; Hiebert, E.
J. Gen. Virol. 73, 3225-3229, 1992
A:Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated from
A:Reference number: JQ1869; MUID:93107858; PMID:1469361
A:Accession: JQ1870
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <ABO>
A:Cross-references: GB:L14460
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 56.0%; Score 200; DB 1; Length 358;
Best Local Similarity 52.9%; Pred. No. 4.4e-15;
Matches 37; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGRGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60
Db 107 TIWGFQIDGRSARGGQGSANDSYAKALNAGVQSALAVLREEQPKDFVLQHNIRSNL 166

QY 61 DRIFDKTPEP 70
Db 167 ERIFAKAPEP 176

RESULT 13
S28360
A11 protein - beet curly top virus
C:Species: beet curly top virus
C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Sep-1999
C:Accession: S28360
R:Stanley, J.; Markham, P.G.; Callis, R.J.; Pinner, M.S.
EMBO J. 5, 1761-1767, 1986
A:Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly top
A:Reference number: S28360
A:Accession: S28360
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-385 <STA>
A:Cross-references: GB:M24597; EMBL:X04144; NID:G210678; PIDN:AAA42751.1; PID:G210679
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 56.0%; Score 200; DB 2; Length 385;
Best Local Similarity 52.9%; Pred. No. 4.8e-15;
Matches 37; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGRGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60
Db 137 TIWGFQIDGRSARGGQGSANDSYAKALNATSLDQALQILKEEQPKDYFLQHHNLNNA 196

QY 61 DRIFDKTPEP 70
Db 197 QKIFQRPPDP 206

RESULT 14
S59885
replication-associated protein C1 - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C>Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
C:Accession: S59885
R:Hong, Y.; Harrison, B.D.
submitted to the EMBL Data Library, February 1995
A:Description: Nucleotide sequences from tomato leaf curl viruses from different countries
d Geminiviruses.
A:Reference number: S58346
A:Accession: S59885
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-360 <HON>
A:Cross-references: EMBL:Z48182; NID:9944838; PIDN:CAA88229.1; PID:9974211
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 54.1%; Score 193; DB 2; Length 360;
Best Local Similarity 57.6%; Pred. No. 2.8e-14;
Matches 38; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 4 WGEFQVDRSGRGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNLDR 63
Db 113 FGVQIDGRSARGGQGSANDAYAEALNSGSKAAALDILREKAPKDFVLOFHNLANLDR 172

QY 64 FDKTPE 69
Db 173 FPPSAB 178

RESULT 15
RQCVC1
A11 protein - tomato yellow leaf curl virus
N:Alternate names: C1 protein
C:Species: tomato yellow leaf curl virus
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: D40779
R:Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.
Virology 185, 151-161, 1991
A:Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single
A:Reference number: A40779; MUID:92024070; PMID:1926771
A:Accession: D40779
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-357 <NAV>
A:Cross-references: GB:X15656; NID:962204; PIDN:CAA33688.1; PID:962207
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 53.5%; Score 191; DB 1; Length 357;
Best Local Similarity 62.3%; Pred. No. 4.7e-14;
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 4 WGEFQVDRSGRGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNLDR 63
Db 111 FGVQIDGRSARGGQGSANDAYAEALNSGSKSEALNILEKAPKDYILOFHNLSNLDR 170

QY 64 F 64
Db 171 F 171

Search completed: December 23, 2003, 09:05:22
Job time: 11 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds
(without alignments)
569.747 Million cell updates/sec

Title: US-09-289-346B-6
Perfect score: 357
Sequence: 1 TLVWGFQVDSARGGCGT.....FAFALNSNLDRIPTKTEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340	95.2	352	1 VAL1_TGMV	P03567 tomato gold
2	240	67.2	361	1 VAL1_PYMV	P27258 potato yell
3	227	63.6	358	1 VAL1_CLVK	P14982 cassava lat
4	227	63.6	358	1 VAL1_CLVN	P14972 cassava lat
5	220	61.6	362	1 VAL1_TYLCU	P36279 tomato yell
6	217	60.8	359	1 VAL1_TYLCU	P38609 tomato yell
7	210	58.8	359	1 VAL1_TYLCM	P27260 tomato yell
8	209	58.5	349	1 VAL1_PHVU	Q06923 pepper huas
9	204	57.1	353	1 VAL1_BGMV	P05175 bean golden
10	203	56.9	355	1 VAL1_BGMV	P21947 abutilon mo
11	200	56.0	358	1 VAL1_BCTV	P14991 beet curly
12	200	56.0	361	1 VAL1_TMOV	Q06657 tomato mott
13	191	53.5	357	1 VAL1_TYLCV	P27259 tomato yell
14	104	29.1	347	1 VAL1_SLCV	Q94048 squash leaf
15	67	18.8	447	1 TBL2_HUMAN	Q944p3 homo sapien
16	64.5	18.1	1713	1 LMA3_HUMAN	Q16787 homo sapien
17	63.5	17.8	1610	1 CCAD_MESAU	Q99244 mesocricetu
18	63.5	17.8	2161	1 CCAD_HUMAN	Q01668 homo sapien
19	63.5	17.8	2203	1 CCAD_RAT	P27732 rattus norv
20	62	17.4	476	1 DGRS_HUMAN	Q96df8 homo sapien
21	62	17.4	479	1 DGRS_MOUSE	Q70279 mus musculu
22	60	16.8	269	1 ORN_YEAST	P54964 saccharomyc
23	60	16.8	295	1 VAL1_TYDVA	P31617 tobacco yell
24	60	16.8	355	1 CRTE_RHOSH	P54905 rhodobacte
25	59.5	16.7	299	1 Y175_HELPJ	Q92mq7 helicobacte
26	59.5	16.7	470	1 RHA RHIME	Q923r2 r diaminobu
27	58.5	16.4	127	1 RS11_LACLA	Q9cdv2 lactococcus
28	58.5	16.4	706	1 Y006_RICPR	Q9zed6 rickettsia
29	58.5	16.4	1232	1 Y005_CABEL	P34643 caenorhabdi
30	58	16.2	207	1 IL6_MARMO	Q35736 marmota mon
31	58	16.2	319	1 LDH2_STAAM	Q99r35 staphylococ
32	58	16.2	319	1 LDH2_STAAM	Q8num9 staphylococ
33	58	16.2	447	1 CDSA_DROME	P56079 d phosphati

34	57.5	16.1	367	1 LHX4_MOUSE	P53776 mus musculu
35	57.5	16.1	491	1 AMPA_ANASP	Q82064 anabaena sp
36	57.5	16.1	844	1 SECA_STACA	P47994 staphylococ
37	57.5	16.1	1852	1 CCAS_CYPCA	P22316 cyprinus ca
38	57	16.0	1502	1 CYP1_YEAST	P12351 saccharomyc
39	57	16.0	1608	1 HLYA_SERMA	P15320 serratia ma
40	56.5	15.8	511	1 HUTH_VIBCH	Q9kseq4 vibrio chol
41	56.5	15.8	2190	1 CCAD_CHICK	O73700 gallus gall
42	56	15.7	258	1 YL48_MYCTU	O06228 mycobacteri
43	56	15.7	408	1 CINA_THEMA	Q985x1 thermotoga
44	56	15.7	492	1 MOT3_MOUSE	O35308 mus musculu
45	56	15.7	492	1 MOT3_RAT	O70461 rattus norv

ALIGNMENTS

RESULT 1					
VAL1_TGMV					
ID VAL1_TGMV	STANDARD;	PRT;	352 AA.		
AC P03567;					
DT 21-JUL-1986 (Rel. 01, Created)					
DT 21-JUL-1986 (Rel. 01, Last sequence update)					
DT 01-JUN-1994 (Rel. 29, Last annotation update)					
DE AL1 protein.					
GN AC1.					
OS Tomato golden mosaic virus (TGMV).					
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.					
OX NCBI_TaxID=10831;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Hamilton W.D.O., Stain V.E., Courts R.H.A., Buck K.W.;					
RT "Complete nucleotide sequence of the infectious cloned DNA components					
RT of tomato golden mosaic virus: potential coding regions and regulatory					
RT sequences.";					
RL EMBO J. 3:2197-2205(1984).					
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.					
CC					
CC This SWISS-PROT entry is copyright. It is produced through a collaboration					
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -					
CC the European Bioinformatics Institute. There are no restrictions on its					
CC use by non-profit institutions as long as its content is in no way					
CC modified and this statement is not removed. Usage by and for commercial					
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/					
CC or send an email to license@isb-sib.ch).					
CC					
CC EMBL; K02029; -; NOT_ANNOTATED_CDS.					
DR PIR; A04170; Q0CVL1.					
DR InterPro; IPR001191; Gemini_AL1.					
DR Pfam; PF00799; Gemini_AL1; 1.					
DR PRINTS; PR00227; GEMCOATALL.					
DR ProDom; PD000736; Gemini_AL1; 1.					
KW ATP-binding.					
FT NP_BIND 223 230 ATP (POTENTIAL).					
SQ SEQUENCE 352 AA; 40332 MW; C33C938E9644B44 CRC64;					

Query Match	95.2%;	Score 340;	DB 1;	Length 352;
Best Local Similarity	95.7%;	Pred. No. 3e-31;		
Matches	67;	Conservative	0;	Mismatches 3;
				Indels 0;
				Gaps 0;
QY	1	TLVWGFQVDSARGGCGTNDAAAEALNASSKEALQIIREKTPKYLPAFALNSNL	60	
Db	111	TLVWGFQVDSARGGCGTNDAAAEALNASSKEALQIIREKTPKYLPAFALNSNL	170	
QY	61	DRIFDKTEP 70		
Db	171	DRIFDKTEP 180		

RESULT 2					
VAL1_PYMV					
ID VAL1_PYMV	STANDARD;	PRT;	361 AA.		
AC P27258;					

```

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE A11 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A.; Coffin R.S.; Roberts E.J.F.; Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D00940; EAA00782.1; -.
CC PIR; J03364; QOCVPT.
CC InterPro; IPR001191; Gemini_A11.
CC Pfam; PF00799; Gemini_A11; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_A11; 1.
CC ATP-binding.
CC NP BIND 222 229 ATP (POTENTIAL).
CC SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;
CC -----
Query Match 67.2%; Score 240; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 7.3e-20;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
CC -----
QY 1 TLVWGFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLFAFALNSNL 60
DB 110 TIEWGLFQIDGRSARGGQQTWVNDAAAEALNASSGTEAKMKIKELPKFLFQYHLSNCL 169
QY 61 DRIFDKTPE 69
DB 170 DRIFDKAPE 178
CC -----
RESULT 3
VAL1 CLV1 STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE A11 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J.; Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----

```

```

CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_A11.
DR Pfam; PF00799; Gemini_A11; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_A11; 1.
KW ATP-binding.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753BE92D69 CRC64;
CC -----
Query Match 63.6%; Score 227; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 2.2e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
CC -----
QY 1 TLVWGFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLFAFALNSNL 60
DB 109 TVEWGQFQIDGRSARGGQSQSANDAYAKALNSGSKSEALNVIRELVKDFVLQFHLNSNL 168
QY 61 DRIFDKTPE 70
DB 169 DRIFQEPAP 178
CC -----
RESULT 4
VAL1 CLV1 STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE A11 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B.; Coates L.; Lowe S.; Richardson K.; Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
RL Nucleic Acids Res. 18:197-198(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X17095; CAA34953.1; -.
CC PIR; S07594; S07594.
CC InterPro; IPR001191; Gemini_A11.
CC Pfam; PF00799; Gemini_A11; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_A11; 1.
CC ATP-binding.
CC NP BIND 220 227 ATP (POTENTIAL).
CC SEQUENCE 358 AA; 40435 MW; 1DB16B80CB2D5E2C CRC64;
CC -----
Query Match 63.6%; Score 227; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 2.2e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
CC -----
QY 1 TLVWGFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLFAFALNSNL 60
DB 109 TVEWGQFQIDGRSARGGQSQSANDAYAKALNSGSKSEALNVIRELVKDFVLQFHLNSNL 168
QY 61 DRIFDKTPE 70
DB 169 DRIFQEPAP 178
CC -----

```

```

RESULT 5
VAL1_TYLCV
ID VAL1_TYLCV STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AL1 protein (C1 protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Rigden J.E., Krake L.R., Mullineaux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
  geminivirus.";
RL J. Gen. Virol. 74:147-151 (1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR PIR; JQ1887; JQ1887.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW NP BIND.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 61.6%; Score 220; DB 1; Length 362;
Best Local Similarity 52.9%; Pred. No. 1.4e-17; Indels 16; Gaps 1;
Matches 45; Conservative 9; Mismatches 15;

QY 1 TLVGEFQVDGRSARGGCGTSDNAAALNASSKEALQIIREKIPEKYLFAFAALNSNL 60
DB 110 TLEWGFQIDGRSARGGCGTSDNAAALNASSKEALQIIREKIPEKYLFAFAALNSNL 169
QY 61 DRI-----FKTPE 69
DB 170 DRIFPPLEVVYSPFLSSSFDRVPE 194

RESULT 6
VAL1_TYLCV
ID VAL1_TYLCV STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (C1 protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Noris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
  from the west Mediterranean basin: the nucleotide sequence of an
  infectious clone from Spain.";
RL Arch. Virol. 135:165-170 (1994).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/annouce/
  or send an email to license@isb-sib.ch).
DR PIR; S22593; S22593.
DR PDB; 1L2M; 18-SEP-02.
DR PDB; 1L5I; 18-SEP-02.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding; 3D-structure.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 40733 MW; 9717BAA07C93EFA7 CRC64;

Query Match 58.8%; Score 210; DB 1; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.9e-16;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDGRSARGGCGTSDNAAALNASSKEALQIIREKIPEKYLFAFAALNSNL 61
DB 111 LEWGTFFQIDGRSARGGCGTSDNAAALNASSKEALQIIREKIPEKYLFAFAALNSNL 170

```

```

CC EMBL; Z25751; CAA81026.1; -.
DR PIR; S39211; S39211.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51BF80A3EC CRC64;

Query Match 60.8%; Score 217; DB 1; Length 359;
Best Local Similarity 59.4%; Pred. No. 3e-17;
Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDGRSARGGCGTSDNAAALNASSKEALQIIREKIPEKYLFAFAALNSNL 61
DB 111 LEWGTFFQIDGRSARGGCGTSDNAAALNASSKEALQIIREKIPEKYLFAFAALNSNL 170
QY 62 RIFDKTPEP 70
DB 171 RVFQVPPAP 179

RESULT 7
VAL1_TYLCM
ID VAL1_TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (C1 protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92107660; PubMed=1840676;
RA Kheyr-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
  Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a
  whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769 (1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/annouce/
  or send an email to license@isb-sib.ch).
DR EMBL; X61153; CAA43466.1; -.
DR PIR; S22593; S22593.
DR PDB; 1L2M; 18-SEP-02.
DR PDB; 1L5I; 18-SEP-02.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding; 3D-structure.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 40733 MW; 9717BAA07C93EFA7 CRC64;

Query Match 58.8%; Score 210; DB 1; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.9e-16;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDGRSARGGCGTSDNAAALNASSKEALQIIREKIPEKYLFAFAALNSNL 61
DB 111 LEWGTFFQIDGRSARGGCGTSDNAAALNASSKEALQIIREKIPEKYLFAFAALNSNL 170

```

```

QY 62 RIFDKTPEP 70
Db 171 KVQVPPAP 179

RESULT 8
VAL1 PHUV STANDARD; PRT; 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AL1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
RT comparison with bipartite geminiviruses.";
RL J. Gen. Virol. 74:2225-2231(1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M10070; AAA46318.1; -
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA79DF6029A34 CRC64;

Query Match 57.1%; Score 204; DB 1; Length 353;
Best Local Similarity 57.1%; Pred. No. 8.8e-16;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIREKIPKYLFAFAALNSNL 60
Db 110 TIEWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIREKIPKYLFAFAALNSNL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFKVPPEP 179

RESULT 10
VAL1 ABMVV STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimmat G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X15983; -; NOT_ANNOTATED_CDS.
DR PIR; A36214; QCCVWL.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.

QY 62 RIFDKTPEP 70
Db 171 KVQVPPAP 179

RESULT 8
VAL1 PHUV STANDARD; PRT; 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AL1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
RT comparison with bipartite geminiviruses.";
RL J. Gen. Virol. 74:2225-2231(1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X70418; CAA49856.1; -
DR PIR; JQ2300; JQ2300.
DR PIR; S31875; S31875.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 39722 MW; DSF4E76CD56370F4 CRC64;

Query Match 58.5%; Score 209; DB 1; Length 349;
Best Local Similarity 57.1%; Pred. No. 2.3e-16;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIREKIPKYLFAFAALNSNL 60
Db 110 TIEWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIREKIPKYLFAFAALNSNL 169
QY 61 DRIFDKTPEP 70
Db 170 NRIFQTPEP 179

RESULT 9
VAL1 BGMV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE AL1 protein (40.2 kDa protein).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]

```

```
FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 355 AA; 40257 MW; 16A2CA8A63251E95 CRC64;

Query Match 56.9%; Score 203; DB 1; Length 355;
Best Local Similarity 55.7%; Pred. No. 1.2e-15;
Matches 39; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TAEWGEFQIDGRSGRGQQTANDSYAKALNAGDVQSALNHLKESQPKDYVLQHNHNSNL 169
Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAP 179

RESULT 11
VAL1_BCTV STANDARD; PRT; 358 AA.
AC P14931;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Ali protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
RT beet curly top virus."
RL EMBL J. 511761-1767(1986).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; L14460; AAC32414.1; -.
DR PIR; JQ1870; JQ1870.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALI.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW NP_BIND 222 229 ATP (BY SIMILARITY).
FT NP_BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match 56.0%; Score 200; DB 1; Length 358;
Best Local Similarity 52.9%; Pred. No. 2.5e-15;
Matches 37; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TAEWGEFQIDGRSGRGQQTANDSYAKALNAGDVQSALNHLKESQPKDYVLQHNHNSNL 169
Qy 61 DRIFDKTPEP 70
Db 170 QKIFRPDP 179

RESULT 12
VAL1_TMOV STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Ali protein.

FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 355 AA; 40257 MW; 16A2CA8A63251E95 CRC64;

Query Match 56.9%; Score 203; DB 1; Length 355;
Best Local Similarity 55.7%; Pred. No. 1.2e-15;
Matches 39; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TAEWGEFQIDGRSGRGQQTANDSYAKALNAGDVQSALNHLKESQPKDYVLQHNHNSNL 169
Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAP 179

RESULT 13
VAL1_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Ali protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component."
RL Virology 185:151-161(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; L14460; AAC32414.1; -.
DR PIR; JQ1870; JQ1870.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALI.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW NP_BIND 222 229 ATP (BY SIMILARITY).
FT NP_BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 8138B65CEAC6950 CRC64;

Query Match 56.0%; Score 200; DB 1; Length 361;
Best Local Similarity 52.9%; Pred. No. 2.6e-15;
Matches 37; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TAEWGEFQIDGRSGRGQQTANDSYAKALNAGDVQSALNHLKESQPKDYVLQHNHNSNL 169
Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAP 179

RESULT 13
VAL1_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Ali protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component."
RL Virology 185:151-161(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; L14460; AAC32414.1; -.
DR PIR; JQ1870; JQ1870.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALI.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW NP_BIND 222 229 ATP (BY SIMILARITY).
FT NP_BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 8138B65CEAC6950 CRC64;

Query Match 56.0%; Score 200; DB 1; Length 361;
Best Local Similarity 52.9%; Pred. No. 2.6e-15;
Matches 37; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TAEWGEFQIDGRSGRGQQTANDSYAKALNAGDVQSALNHLKESQPKDYVLQHNHNSNL 169
Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAP 179
```



```

DR EMBL; X15656; CAA33688.1; -.
DR PIR; D40779; QOCVCI.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOAT1.
DR ProDom; PD000736; Gemini_AL1.1.
KW ATP-binding.
FT NP BIND 219 226 ATP (POTENTIAL).
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match 53.5%; Score 191; DB 1; Length 357;
Best Local Similarity 62.3%; Pred. No. 2.7e-14;
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 4 WGEFQVGRSARGGCGTSDNDAAEALNASSKEALQIREKIPKYLFAFALNSNLDRI 63
Db 111 FGVQIDGRSARGGCGQANDAYAEALNSGSKSEALNLIKERAKPKDYILQPHNLSNLDRI 170

Qy 64 F 64
Db 171 F 171

RESULT 14
ID VAL1_SLCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G.; Lardias I.B.;
RT Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype."
RL Virology 180:58-69(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M38183; AAC32410.1; ALT_INIT.
CC PIR; C36785; QOCVSI.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1.1.
CC PRINTS; PR00227; GEMCOAT1.
CC ProDom; PD000736; Gemini_AL1.1.
KW ATP-binding.
FT NP BIND 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDAEBDD122110E CRC64;

Query Match 29.1%; Score 104; DB 1; Length 347;
Best Local Similarity 34.8%; Pred. No. 0.0002;
Matches 23; Conservative 14; Mismatches 25; Indels 4; Gaps 1;

Qy 5 GEFQVGRSARGGCGTSDNDAAEALNASSKEALQIREKIPKYLFAFALNSNLDRI 64
Db 116 GQYKVG-----GSKSNKDDVTHNAVAGSAGEALDIKAGDKTFIVYHNLNANVERLF 171

Qy 65 DKTEPE 70
Db 172 QKPPEP 177

```

RESULT 15

```

TBL2_HUMAN
ID TBL2_HUMAN STANDARD; PRT; 447 AA.
AC Q9Y4F5; Q9U0E2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transducin beta-like 2 protein (WS beta-transducin repeats protein)
DE (WS-beta2TP) (Williams-Beuren syndrome chromosome region 13 protein).
GN TBL2 OR WBSCE13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20044626; PubMed=10575226;
RA Perez Jurado L.A.; Wang Y.-K.; Francke U.; Cruces J.;
RT "TBL2, a novel transducin family member in the WBS deletion:
RT characterization of the complete sequence, genomic structure,
RT transcriptional variants and the mouse ortholog."
RL Cytogenet. Cell Genet. 86:277-284(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S.; Weil B.; Wellenreuther R.; Gassenhuber J.; Glassl S.;
RA Ansorge W.; Boecker M.; Bloeker H.; Bauersachs S.; Blum H.;
RA Lauber J.; Dueterhoeft A.; Beyer A.; Koehrer K.; Strack N.;
RA Mewes H.-W.; Ottenwelder B.; Obermaier B.; Tampe J.; Heubner D.;
RA Wambutt R.; Korn B.; Klein M.; Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs."
RL Genome Res. 11:422-435(2001).
RN [3]
RP SEQUENCE OF 14-447 FROM N.A.
RX MEDLINE=99075645; PubMed=9860302;
RA Meng X.; Lu X.; Li Z.; Green E.D.; Massa H.; Trask B.J.; Morris C.A.;
RA Keating M.T.;
RT "Complete physical map of the common deletion region in Williams
RT syndrome and identification and characterization of three novel
RT genes."
RL Hum. Genet. 103:590-599(1998).
CC -!- DISEASE: Haploinsufficiency of TBL2 may be the cause of certain
CC cardiovascular and musculo-skeletal abnormalities observed in
CC Williams-Beuren syndrome (WBS) [MIM:194050], a rare developmental
CC disorder. It is a contiguous gene deletion syndrome involving
CC genes from chromosome band 7q11.23.
CC -!- SIMILARITY: Contains 7 WD repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF097484; AAF06823.1; -.
CC EMBL; AF097485; AAF06824.1; -.
CC EMBL; AF080162; CAB45751.1; -.
CC EMBL; AF056183; AAD28083.1; ALT_INIT.
CC PIR; T12544; T12544.
CC Genew; HGNC:11586; TBL2.
CC MIM; 605842; -.
CC MIM; 194050; -.
CC InterPro; IPR001680; WD40.
CC Pfam; PF00400; WD40; 5.
CC PRINTS; PR00320; GPROTEINBRPT.
CC ProDom; PD000018; WD40; 2.
CC SMART; SM00320; WD40; 5.

```

DR PROSITE; PS00678; WD REPEATS 1; 1.
DR PROSITE; PS00082; WD REPEATS 2; 3.
DR PROSITE; PS0294; WD REPEATS_REGION; 1.
KW Repeat; WD repeat; Williams-Beuren syndrome.
FT REPEAT 88 127 WD 1.
FT REPEAT 134 174 WD 2.
FT REPEAT 186 226 WD 3.
FT REPEAT 228 267 WD 4.
FT REPEAT 277 316 WD 5.
FT REPEAT 329 367 WD 6.
FT REPEAT 371 409 WD 7.
SQ SEQUENCE 447 AA; 49797 MW; B260087E1A71D3F9 CRC64;

Query Match 18.8%; Score 67; DB 1; Length 447;
Best Local Similarity 32.1%; Pred.No. 4.3;
Matches 18; Conservative 11; Mismatches 23; Indels 4; Gaps 1;

QY 12 RSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFAF---AALNSNLDRI 63
Db ||||| : : : : : ||| : : : : : ||| : : : : :
38 RSGRPACQKANGFPDPKSSGSKKQYQYRIKEKTPQHNFTHRLLAALKSHSGNI 93

Search completed: December 23, 2003, 08:57:39
Job time : 6.77778 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 25.3333 Seconds
(without alignments)
713.040 Million cell updates/sec

Title: US-09-289-346B-6

Perfect score: 357

Sequence: 1 TLVWGSEFQVDSRGSGCQT.....FAPALNSNLDRIPTKPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291	81.5	351	12	Q91R10 tomato seve
2	289	81.0	352	12	Q9E000 tomato rugo
3	281	78.7	232	12	Q8QPV3 tomato chlo
4	272	76.2	226	12	Q9WHF6 tomato mild
5	272	76.2	226	12	Q09727 leonurus mo
6	270	75.6	361	12	Q67574 bean golden
7	268	75.1	225	12	Q9QDB1 cowpea gold
8	268	75.1	314	12	Q9ELT8
9	268	75.1	364	12	Q9Q855
10	265	74.2	185	12	Q98693
11	261	73.1	235	12	Q8QPU4
12	260	72.8	208	12	Q8JLY3 potato infe
13	260	72.8	289	12	Q8JLY3 potato yell
14	257	72.0	149	12	F88975
15	257	72.0	233	12	Q9YLA4 macroptiliu
16	256	71.7	361	12	Q8JMJ4 potato yell

17	254	71.1	360	12	Q8QMH4
18	252	70.6	361	12	Q8QVH0
19	251	70.3	234	12	Q39180 geminivirid
20	249	69.7	223	12	Q8QPU7
21	248	69.5	190	12	Q9Z089
22	248	69.5	190	12	Q9Z084 tobacco lea
23	247	69.2	190	12	Q9W827
24	247	69.2	208	12	Q9Z0C4
25	247	69.2	359	12	Q91M88
26	247	69.2	359	12	Q8JVE8
27	245	68.6	208	12	Q9Z0C0
28	245	68.6	208	12	Q9Z0B8
29	243	68.1	208	12	Q9Z086
30	242	67.8	203	12	Q9Z083
31	242	67.8	349	12	Q88888
32	242	67.8	363	12	Q73577
33	239	66.9	208	12	Q9Z0A0
34	238	66.7	208	12	Q9Z0C6
35	237	66.4	359	12	Q91B86
36	237	66.4	360	12	Q9DX10
37	235	65.8	363	12	Q72719
38	235	65.8	363	12	Q72705
39	234	65.5	190	12	Q9Z086
40	233	65.3	362	12	Q56816
41	232	65.0	359	12	Q9YZV4
42	232	65.0	359	12	Q9YUX7
43	232	65.0	359	12	Q9YL27
44	232	65.0	359	12	Q9YZV2
45	232	65.0	364	12	Q8V5Z4

ALIGNMENTS

RESULT 1

Q91R10 ID Q91R10 PRELIMINARY; PRT; 351 AA.
AC Q91R10, (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Rep protein.
GN ACI.
OS Tomato severe rugose virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=158463;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Minas Gerais;
RA Rezende W.L., Goulart L.R., Parreira K.S., Figueiredo J.E.F.;
RT "The full-length DNA-A nucleotide sequence of a novel tomato-infecting
RL begomovirus, Tomato severe rugose virus, in Brazil."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029750; AAK50357.1; -
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 351 AA; 40122 MW; 87F937A4F873B6CF CRC64;

Query Match 81.5%; Score 291; DB 12; Length 351;
Best Local Similarity 78.6%; Pred. No. 6.6e-26;
Matches 55; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TLVWGSEFQVDSRGSGCQTSDAAAEALNASKERALQIIRKIPKYLFAFALNSNL 60

Db 111 TIWGFQIDGRGARGCCQTANDAAAEALNASKERALQIIRKIPKYLFAFALNSNL 170

Qy 61 DRIPDKTPEP 70

Db 171 DRIFARAPEP 180


```

SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;
Query Match 76.2%; Score 272; DB 12; Length 361;
Best Local Similarity 77.1%; Pred. No. 6.7e-24;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
Db 111 TVWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 170

QY 61 DRIFDKTPEP 70
Db 171 DRIFAKAPEP 180

RESULT 6
Q67574
ID Q67574 PRELIMINARY; PRT; 361 AA.
AC Q67574;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Putative replicative protein.
GN Ali.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales P.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration.";
RL Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
RT hybridization probes and aspects of bean golden mosaic in Brazil.";
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus.";
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M88686; AAA46312.1; -.
DR InterPro; IPR001191; Geminini_A11.
DR Pfam; PF00799; Geminini_A11; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Geminini_A11; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 75.6%; Score 270; DB 12; Length 361;
Best Local Similarity 76.1%; Pred. No. 2e-23;
Matches 51; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 4 WGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFALNSLDRI 63
Db 113 WGHFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKFLFQYHNLSSLDRI 172

QY 64 FDKTPEP 70
Db 173 FTKAPDP 179

RESULT 7
Q9QDB1
ID Q9QDB1 PRELIMINARY; PRT; 225 AA.
AC Q9QDB1;

```

```

DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGMV-BR;
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RT Brazil.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF198708; AAF06318.1; -.
DR InterPro; IPR001191; Geminini_A11.
DR Pfam; PF00799; Geminini_A11; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Geminini_A11; 1.
FT NON_TER 225
SQ SEQUENCE 225 AA; 25766 MW; 1089CB8BD15B5D CRC64;

Query Match 75.1%; Score 268; DB 12; Length 225;
Best Local Similarity 76.1%; Pred. No. 2e-23;
Matches 51; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 4 WGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFALNSLDRI 63
Db 113 WGHFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKFLFQYHNLSSLDRI 172

QY 64 FDKTPEP 70
Db 173 FKKEPEP 179

RESULT 8
Q9ELT8
ID Q9ELT8 PRELIMINARY; PRT; 314 AA.
AC Q9ELT8;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Replication associated protein.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288237; AAG01006.1; -.
DR InterPro; IPR001191; Geminini_A11.
DR Pfam; PF00799; Geminini_A11; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Geminini_A11; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 75.1%; Score 268; DB 12; Length 314;
Best Local Similarity 79.4%; Pred. No. 2.9e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TITWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKFLFQYHNLVSNL 169

```

```

Qy 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 9
Q9QS55 PRELIMINARY; PRT; 364 AA.
AC Q9QS55;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Vaiverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Vaiverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0(1999).
DR EMBL; AF104036; AAD47173.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Geminini_AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D5E CRC64;

Query Match 75.1%; Score 268; DB 12; Length 364;
Best Local Similarity 79.4%; Pred. No. 3.5e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 TLWGEFQVDRSGRGCGQTSNDAAAFALNASSKEALQIIREKIPKYLFAFALNSNL 60
Db 110 TIIWGEFQVDRSGRGCGQTSNDAAAFALNASSKEALQIIREKIPKYLFAFALNSNL 169
Qy 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica;
RA Roye M.E., McLaughlin W.A., Nakha N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed species Sida spp, Macroptilium lathyroides, and Wissadula amplissima from Jamaica.";
RL Plant Dis. 81:1251-1258(1997).
DR EMBL; U67926; AAB97865.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.

RESULT 11
Q8QPU4 PRELIMINARY; PRT; 235 AA.
AC Q8QPU4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG-Bil;
RA Ribeiro S.G., Ambrozecivicius L.P., de Avila A.C., Calegario R.P.,
RA Fernandes J.J., Lima M.P., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049208; AAL82833.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR ProDom; PD000736; Geminini_AL1; 1.
FT NON TER 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BE0DD9C810 CRC64;

Query Match 73.1%; Score 261; DB 12; Length 235;
Best Local Similarity 73.1%; Pred. No. 1.4e-22;
Matches 49; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 4 WGEFQVDRSGRGCGQTSNDAAAFALNASSKEALQIIREKIPKYLFAFALNSNL 63
Db 113 WGIFQIDGRSARGCGQTSNDAAAFALNASSKEALQIIREKIPKYLFAFALNSNL 172
Qy 64 FKTPPEP 70
Db 173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

```

```
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Jamaican;
RL      Roye M.E.;
RR      Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
RA      EMBL: U75278; AAB36919.1; -.
RD      InterPro: IPR001191; Gemini_AL1.
DR      Pfam: PF00799; Gemini_AL1; 1.
DS      PRINTS: PR00227; GEMCORTALI.
DT      ProDom: PD000736; Gemini_AL1; 1.
DZ      NON TER          1
FT      NON TER         149
SQ      SEQUENCE        149 AA;  16785 MW;  B4CF5EED4C9CD508 CRC64;

Query Match              72.0%; Score 257; DB 12; Length 149;
Best Local Similarity    68.6%; Pred.No.2.4e-22;
Matches   48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy      1 TLVGFGEFQVDGRSGRGCGQTSSNDAAAEALNASKKEAQIIRIKIPKYLFAPAALNSNL 60
Db       : |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy     61 DRIFDKTPEP 70
Db     112 DRIEFMKDPEP 121

RESULT 15
QYILA4 PRELIMINARY; PRT; 233 AA.
ID QYILA4 AC QYILA4;
AC QYILA4 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DI 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geniniviridae; Begomovirus.
OX NCBI_Taxid=51676;
RN RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Jamaica strain 1;
RA Roye M.E.;
RD "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica.";
RE Submitted (Oct-1998) to the EMBL/GenBank/DDBJ databases.
RZ [2]
RN RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Jamaica strain 1;
RA Roye M.E., McLaughlin W.A., Maxwell D.P.;
RD "Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica.";
RE Submitted (Oct-1998) to the EMBL/GenBank/DDBJ databases.
DL EMBL: AF098940; AAD17850.1; -
DR InterPro: IPR001191; Gemini_AL1.
DD Pfam: PF00799; Gemini_AL1; 1.
DS PRINTS: PR00227; GEMCORTALI.
DT ProDom: PD000736; Gemini_AL1; 1.
DZ NON TER          233
FT NON TER         233 AA;  26356 MW;  AA490AF4D2166A02 CRC64;

Query Match              72.0%; Score 257; DB 12; Length 233;
Best Local Similarity    68.6%; Pred.No.4e-22;
Matches   48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy      1 TLVGFGEFQVDGRSGRGCGQTSSNDAAAEALNASKKEAQIIRIKIPKYLFAPAALNSNL 60
Db     110 TIENGVFQIDGSRARGCGQTSSNDAAAEALNSGTKEAMRVKEKLPEKFLEYHNLSNL 169
Qy     61 DRIFDKTPEP 70
Db     170 DRIEFMKDPEP 179
```

Search completed: December 23, 2003, 09:03:36
Job time : 26.3333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds
(without alignments)
340.128 Million cell updates/sec

Title: US-09-289-346B-7
Perfect score: 359
Sequence: 1 TLVGFQVQDRSARGCQT.....FOFHNLNSALAAIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03:*

1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*

9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*

10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*

11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*

12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*

13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*

14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*

15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	100.0	70	21 AAB18683	Mutant peptide der
2	342	95.3	70	21 AAB18677	Peptide fragment f
3	342	95.3	356	21 AAB18687	Amino acid sequenc
4	334	93.0	70	21 AAB18685	Mutant peptide der
5	331	92.2	70	21 AAB18688	Mutant peptide der
6	330	91.9	70	21 AAB18692	Mutant peptide der
7	328	91.4	70	21 AAB18684	Mutant peptide der
8	328	91.4	70	21 AAB18690	Mutant peptide der
9	327	91.1	70	21 AAB18678	Mutant peptide der

10	327	91.1	70	21 AAB18686	Mutant peptide der
11	326	90.8	70	21 AAB18689	Mutant peptide der
12	324	90.3	70	21 AAB18680	Mutant peptide der
13	324	90.3	70	21 AAB18691	Mutant peptide der
14	321	89.4	70	21 AAB18681	Mutant peptide der
15	318	88.6	70	21 AAB18682	Mutant peptide der
16	310	86.4	70	21 AAB18679	Mutant peptide der
17	213	59.3	353	18 AAW34338	Bean golden mosaic
18	213	59.3	353	18 AAW34332	Bean golden mosaic
19	213	59.3	353	18 AAW34333	Bean golden mosaic
20	213	59.3	353	18 AAW34334	Bean golden mosaic
21	213	59.3	353	18 AAW34335	Bean golden mosaic
22	211	58.8	353	8 AAP70407	ORF 4 gene product
23	211	58.8	359	17 AAR88870	Sardinian tomato Y
24	211	58.8	359	17 AAR88871	Sardinian tomato Y
25	211	58.8	359	17 AAR88872	Sardinian tomato Y
26	211	58.8	361	18 AAW34336	Tomato mottle viru
27	211	58.8	361	18 AAW34324	Tomato mottle viru
28	211	58.8	361	18 AAW34325	Tomato mottle viru
29	211	58.8	361	18 AAW34326	Tomato mottle viru
30	208.5	58.1	361	8 AAP70562	Product of ORF 4 f
31	201.5	56.1	50	23 AAO22043	Retinoblastoma-bin
32	194	54.0	362	19 AAW56495	Tobacco leaf curl
33	193	53.8	357	18 AAW34329	Tomato yellow leaf
34	193	53.8	357	18 AAW34330	Tomato yellow leaf
35	193	53.8	357	18 AAW34331	Tomato yellow leaf
36	185	51.5	357	18 AAW34337	Tomato yellow leaf
37	104	29.0	142	24 ABP58120	Tomato yellow leaf
38	68	18.9	447	21 AAY99659	Human GTPase assoc
39	68	18.9	447	21 AAY87089	Human secreted pro
40	68	18.9	447	21 AAY66744	Membrane-bound pro
41	68	18.9	447	21 AAY50947	Human adult aorta
42	68	18.9	447	22 AAU29150	Human PKO polypept
43	68	18.9	447	22 AAM93267	Human polypeptide,
44	68	18.9	447	22 AAE06066	Human gene 26 enco
45	68	18.9	447	22 AAE65267	Human PRO1125 (UNQ

ALIGNMENTS

RESULT 1

AB18683

ID AAB18683 standard; peptide; 70 AA.

XX AC AAB18683;

XX DT 22-JAN-2001 (first entry)

XX DE Mutant peptide derived from amino acids 110-179 of Rep (Al1) protein.

XX KW Geminivirus; replication protein; Rep protein; Al1; transgenic plant;

XX KW ribosome binding region; resistance; geminivirus infection.

XX OS Synthetic.

XX OS Tomato golden mosaic virus.

XX FH Key Location/Qualifiers

FT FT Misc-difference 59 /note= "wild type residue replaced with Ala"

FT FT Misc-difference 61 /note= "wild type residue replaced with Ala"

FT FT Misc-difference 62 /note= "wild type residue replaced with Ala"

XX WO200054573-Al.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 PI WPI; 2000-618851/59.
 DR
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 FT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 XX
 PS Claim 53; Page 45; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 100.0%; Score 359; DB 21; Length 70;
 Best Local Similarity 100.0%; Pred. No. 1e-38;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVQGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
 DB 1 TLVWGEFQVQGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
 QY 61 AAIFDKTPEP 70
 DB 61 AAIFDKTPEP 70
 RESULT 2
 AAB18677
 ID AAB18677 standard; peptide; 70 AA.
 AC AAB18677;
 XX
 DT 22-JAN-2001 (first entry)
 DE Peptide fragment from Rep protein of TGMV (amino acids 110-179).
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Tomato golden mosaic virus.
 XX
 PN WO200054573-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX
 DR WPI; 2000-618851/59.
 PT

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 FT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 XX
 PS Disclosure; Page 18; 73pp; English.
 XX
 CC The present sequence is derived from a geminivirus replication (Rep)
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
 CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
 CC with other viral and host proteins. Mutants of the AL1 protein are used
 CC to produce transgenic plants. The mutation in AL1 is present in a
 CC ribosome binding region, and expression of mutant AL1 protein imparts
 CC increased resistance to geminivirus infection in the plant. Mutant AL1
 CC proteins are useful for producing plants having increased resistance or
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 CC beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 95.3%; Score 342; DB 21; Length 70;
 Best Local Similarity 95.7%; Pred. No. 1.6e-36;
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVQGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
 DB 1 TLVWGEFQVQGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
 QY 61 AAIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 3
 AAB18687
 ID AAB18687 standard; peptide; 356 AA.
 AC AAB18687;
 XX
 DT 22-JAN-2001 (first entry)
 DE Amino acid sequence of a geminivirus replication protein of TGMV.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Tomato golden mosaic virus.
 XX
 PN Key Location/Qualifiers
 FT Misc-difference 354 /note= "unspecified amino acid"
 FT WO200054573-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX
 DR WPI; 2000-618851/59.
 XX
 PT Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX
 PS Disclosure; Page 47-48; 73pp; English.
 XX
 CC The present sequence represents a geminivirus replication (Rep)
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
 CC catalyses cleavage and ligation of single-stranded DNA,
 CC with other viral and host proteins. Mutants of the AL1 protein are used
 CC to produce transgenic plants. The mutation in AL1 is present in a
 CC ribosome binding region, and expression of mutant AL1 protein imparts
 CC increased resistance to geminivirus infection in the plant. Mutant AL1
 CC proteins are useful for producing plants having increased resistance or
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 CC beet curly top virus.
 XX
 XX
 SQ Sequence 356 AA;

Query Match 95.3%; Score 342; DB 21; Length 356;
 Best Local Similarity 95.7%; Pred. No. 1.3e-35;
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TLVWGFQVGRSARGGCGTSDNDAALNASSKEALQIIRKIKPKYLFQFHNLSAL 60
 Db 110 TLVWGFQVGRSARGGCGTSDNDAALNASSKEALQIIRKIKPKYLFQFHNLSNL 169
 QY 61 AAIFDKTPEP 70
 Db 170 DRIFDKTPEP 179

RESULT 4
 AAB18685
 ID AAB18685 standard; peptide; 70 AA.
 AC AAB18685;
 XX
 XX 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 10
 FT /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-Al.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI WPI; 2000-618851/59.
 DR
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 XX
 PS Claim 53; Page 46; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX
 SQ Sequence 70 AA;

Query Match 93.0%; Score 334; DB 21; Length 70;
 Best Local Similarity 94.3%; Pred. No. 1.8e-35;
 Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TLVWGFQVGRSARGGCGTSDNDAALNASSKEALQIIRKIKPKYLFQFHNLSAL 60
 Db 1 TLVWGFQVGRSARGGCGTSDNDAALNASSKEALQIIRKIKPKYLFQFHNLSNL 60
 QY 61 AAIFDKTPEP 70
 Db 61 DRIFDKTPEP 70

RESULT 5
 AAB18688
 ID AAB18688 standard; peptide; 70 AA.
 AC AAB18688;
 XX
 XX 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 19
 FT /note= "wild type residue replaced with Ala"
 FT Misc-difference 20
 FT /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-Al.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI WPI; 2000-618851/59.
 DR
 XX Transgenic plants with increased resistance to geminivirus infection
 PT

PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX -
 XX Disclosure; Page 48; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;

Query Match 92.2%; Score 331; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 4.3e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVGRSGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
 DB 1 TLVWGEFQVGRSGGCGAASNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
 QY 61 AAFDKTPEP 70
 DB 61 DRIFDKTPEP 70

RESULT 6
 AAB18692
 ID AAB18692 standard; peptide; 70 AA.
 XX
 AC AAB18692;
 XX
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 66 /note= "wild type residue replaced with Ala"
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"
 FT
 XX
 XX WO2000054573-Al.
 XX
 XX
 PD 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX

PT Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX -
 XX Disclosure; Page 50; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 91.9%; Score 330; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 5.9e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVGRSGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
 DB 1 TLVWGEFQVGRSGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
 QY 61 AAFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 7
 AAB18684
 ID AAB18684 standard; peptide; 70 AA.
 XX
 AC AAB18684;
 XX
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 7 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"
 FT
 XX
 XX WO2000054573-Al.
 XX
 XX
 PD 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant All protein with a mutation in the Rb binding region
 PT
 XX
 PS Claim 52; Page 45; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as All. All binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the All
 CC protein are used to produce transgenic plants. The mutation in All is
 CC present in a ribosome binding region, and expression of mutant All
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant All proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;

Query Match 91.4%; Score 328; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 1.1e-34;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGCQTSNDAAALNASSKEKALQIIREKIPEKYLFOFHNLSAL 60
 Db 1 TLVWGEAANDGRSGRGCGCQTSNDAAALNASSKEKALQIIREKIPEKYLFOFHNLSNL 60

QY 61 AAIFDKTPEP 70
 Db 61 DRIFDKTPEP 70

RESULT 8
 AAB18690
 ID AAB18690 standard; peptide; 70 AA.

AC AAB18690;
 XX
 DT 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (All) protein.
 DE Geminivirus; replication protein; Rep protein; All; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.
 OS Tomato golden mosaic virus.

XX Key Location/Qualifiers
 FH Misc-difference 27 /note= "wild type residue replaced with Ala"
 FT Misc-difference 30 /note= "wild type residue replaced with Ala"
 FT Misc-difference 30 /note= "wild type residue replaced with Ala"

XX WO2000054573-Al.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX

DR WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant All protein with a mutation in the Rb binding region
 PT
 XX
 PS Disclosure; Page 49; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as All. All binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the All
 CC protein are used to produce transgenic plants. The mutation in All is
 CC present in a ribosome binding region, and expression of mutant All
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant All proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;

Query Match 91.4%; Score 328; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 1.1e-34;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGCQTSNDAAALNASSKEKALQIIREKIPEKYLFOFHNLSAL 60
 Db 1 TLVWGEAANDGRSGRGCGCQTSNDAAALNASSKEKALQIIREKIPEKYLFOFHNLSNL 60

QY 61 AAIFDKTPEP 70
 Db 61 DRIFDKTPEP 70

RESULT 9
 AAB18678

ID AAB18678 standard; peptide; 70 AA.

AC AAB18678;

XX
 DT 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (All) protein.
 DE Geminivirus; replication protein; Rep protein; All; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.
 OS Tomato golden mosaic virus.

XX Key Location/Qualifiers
 FH Misc-difference 12 /note= "wild type residue replaced with Ala"
 FT Misc-difference 13 /note= "wild type residue replaced with Ala"
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"

XX WO2000054573-Al.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

```

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX XX WPI; 2000-618851/59.
XX DR
XX XX Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX FT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT
XX PS Claim 53; Page 42-43; 73pp; English.
XX XX
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 91.1%; Score 327; DB 21; Length 70;
Best Local Similarity 91.4%; Pred No. 1.4e-34;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 TLVNGEFQVDSARGGCGTSDNAAALNASSKEALQIIREKIPKYLQFHNLSAL 60
Db 1 TLVNGEFQVDSARGGCGTSDNAAALNASSKEALQIIREKIPKYLQFHNLSNL 60
Qy 61 AAFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 10
ID AAB18686 standard; peptide; 70 AA.
XX AC AAB18686;
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX XX Key Location/Qualifiers
XX FT Misc-difference 24 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 25 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 26 /note= "wild type residue replaced with Leu"
XX FT
XX PN WO200054573-A1.
XX XX 21-SEP-2000.
XX XX 15-MAR-2000; 2000WO-US06759.
XX XX 18-MAR-1999; 99US-0125004.

```

```

PR 09-APR-1999; 99US-0289346.
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX XX
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX XX WPI; 2000-618851/59.
XX DR
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT
XX PS Claim 53; Page 46; 73pp; English.
XX XX
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 91.1%; Score 327; DB 21; Length 70;
Best Local Similarity 91.4%; Pred No. 1.4e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 TLVNGEFQVDSARGGCGTSDNAAALNASSKEALQIIREKIPKYLQFHNLSAL 60
Db 1 TLVNGEFQVDSARGGCGTSDNLLLEALNASSKEALQIIREKIPKYLQFHNLSNL 60
Qy 61 AAFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 11
ID AAB18689 standard; peptide; 70 AA.
XX AC AAB18689;
XX XX 22-JAN-2001 (first entry)
XX DT Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX XX Key Location/Qualifiers
XX FT Misc-difference 22 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX FT
XX PN WO200054573-A1.
XX XX 21-SEP-2000.
XX XX 15-MAR-2000; 2000WO-US06759.
XX XX

```

```

PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UUNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
FT comprise a nucleic acid construct containing a nucleic acid sequence
FT encoding a mutant ALI protein with a mutation in the Rb binding region
FT
XX
XX Disclosure; Page 48-49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as ALI. ALI binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the ALI
CC protein are used to produce transgenic plants. The mutation in ALI is
CC present in a ribosome binding region, and expression of mutant ALI
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant ALI proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, bean dwarf mosaic virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 90.8%; Score 326; DB 21; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.9e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEALQIIREKIPKYLFOFHNLSAL 60
DB 1 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEALQIIREKIPKYLFOFHNLSAL 60
QY 61 AAFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 12
AAB18680
ID AAB18680 standard; peptide; 70 AA.
XX
AC AAB18680;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.
XX
XX Geminivirus; replication protein; Rep protein; ALI; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 42 /note= "wild type residue replaced with Ala"
FT Misc-difference 43 /note= "wild type residue replaced with Ala"
FT Misc-difference 44 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
PD 21-SEP-2000.

```

```

XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UUNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
FT comprise a nucleic acid construct containing a nucleic acid sequence
FT encoding a mutant ALI protein with a mutation in the Rb binding region
FT
XX
XX Claim 52; Page 43-44; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as ALI. ALI binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the ALI
CC protein are used to produce transgenic plants. The mutation in ALI is
CC present in a ribosome binding region, and expression of mutant ALI
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant ALI proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, bean dwarf mosaic virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 90.3%; Score 324; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 3.5e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEALQIIREKIPKYLFOFHNLSAL 60
DB 1 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEALQIIREKIPKYLFOFHNLSAL 60
QY 61 AAFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 13
AAB18691
ID AAB18691 standard; peptide; 70 AA.
XX
AC AAB18691;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.
XX
XX Geminivirus; replication protein; Rep protein; ALI; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 34 /note= "wild type residue replaced with Ala"
FT Misc-difference 35 /note= "wild type residue replaced with Ala"
FT Misc-difference 36 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
PD 21-SEP-2000.

```

```

PN WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Disclosure; Page 49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 90.3%; Score 324; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 3.5e-34;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
XX Db 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
XX
XX QY 61 AAIFDKTPEP 70
XX Db 61 DRIFDKTPEP 70
XX
XX RESULT 14
XX AAB18681
XX ID AAB18681 standard; peptide; 70 AA.
XX AC AAB18681;
XX XX
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX XX
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KM ribosome binding region; resistance; geminivirus infection.
XX XX
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 47
XX FT /note= "wild type residue replaced with Ala"
XX FT Misc-difference 48
XX FT /note= "wild type residue replaced with Ala"
XX FT

```

```

FT Misc-difference 49
FT /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 52; Page 44; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 89.4%; Score 321; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 8.6e-34;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
XX Db 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
XX
XX QY 61 AAIFDKTPEP 70
XX Db 61 DRIFDKTPEP 70
XX
XX RESULT 15
XX AAB18682
XX ID AAB18682 standard; peptide; 70 AA.
XX AC AAB18682;
XX XX
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX XX
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KM ribosome binding region; resistance; geminivirus infection.
XX XX
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 52

```


FT	/note= "wild type residue replaced with Ala"
FT	Misc-difference 54
FT	/note= "wild type residue replaced with Ala"
FT	Misc-difference 55
FT	/note= "wild type residue replaced with Ala"

```

...
/ note= "wild type residue replaced with Ala"
...

```

Misc-difference 55

```
/note= "wild type residue replaced with Ala"
```

XX PN WO200054573-A1.

XX
PD 21-SEP-2000.XX
PF 15-MAR-2000: 20

XX
07-13-00; 20

PR 18-MAR-1999;
PR 09-APR-1999;

XX
PA (UYNC--} UNIV NOXX
PI Hanley-Bowdoin

XX
DB
WDT: 2000 0100F
MURPHY-BOWDOIN

DR 58879-0007; 2000-61885

PT Transgenic plants comprise a nucle

PT encoding a mutant

XX
pg 27

Ps Claim 53; Page 1

CC The present sequ
CC geminivirus rep

CC double-stranded
CC DNA, and interac

protein are used present in a vil

present in a film
protein imparts

CC plant. Mutant Al
CC increased resist

CC	tomato golden mosaic virus.
CC	tomato leaf curl virus.

cassava mosaic v

CC virus, bean dwarf
CC virus, cotton leaf

XX	Sequence	70 A
SQ		

Query Match

Best Local Similarity
Matches 64: Cons

Matchless 67; Collins

QY I TLVGEF
|||||

Db 1 TLVWGEF

Qy 61 AAI FDKT
| | | | |

Db 61 DRIEDKT

Search completed: Dec
Job time : 32.6667 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 11.6667 Seconds
(without alignments)
253.865 Million cell updates/sec

Title: US-09-289-346B-7

Perfect score: 359

Sequence: 1 TLWGEFQVDSARGGCQT.....FQHNLNSALAAIFDKTEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	59.3	353	3	US-08-838-151A-44
2	213	59.3	353	3	US-08-838-151A-46
3	213	59.3	353	3	US-08-838-151A-49
4	213	59.3	353	3	US-08-838-151A-52
5	213	59.3	353	3	US-08-838-151A-55
6	211	58.8	359	3	US-08-809-103B-2
7	211	58.8	359	3	US-08-809-103B-4
8	211	58.8	359	3	US-08-809-103B-6
9	211	58.8	359	3	US-08-809-103B-8
10	211	58.8	361	3	US-08-838-151A-2
11	211	58.8	361	3	US-08-838-151A-4
12	211	58.8	361	3	US-08-838-151A-6
13	211	58.8	361	3	US-08-838-151A-8
14	193	53.8	357	3	US-08-838-151A-24
15	193	53.8	357	3	US-08-838-151A-27
16	193	53.8	357	3	US-08-838-151A-30
17	185	51.5	357	3	US-08-838-151A-20
18	68	18.9	447	4	US-09-996-243-369
19	68	18.9	447	4	US-09-482-273-128
20	68	18.9	456	4	US-09-482-273-229
21	63.5	17.7	244	4	US-09-328-352-4541
22	63.5	17.7	2161	1	US-07-745-206A-2
23	63.5	17.7	2161	1	US-08-455-543A-49
24	63.5	17.7	2161	1	US-08-455-543A-51
25	63.5	17.7	2161	2	US-08-233-305C-49
26	63.5	17.7	2161	2	US-08-233-305C-51
27	63.5	17.7	2161	2	US-08-311-363-2

Sequence 4, Appli
Sequence 14, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 34, Appli
Sequence 51, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 29, Appli
Sequence 30, Appli
Sequence 5120, Ap
Sequence 4834, Ap
Sequence 20895, A
Sequence 6, Appli
Sequence 6, Appli
Patent No. 5422248

62.5 17.4 512 4 US-09-319-588C-4
60.5 16.9 131 3 US-08-838-151A-14
59 16.4 293 4 US-09-414-276-3
59 16.4 335 4 US-09-414-276-6
59 16.4 531 4 US-08-976-063B-34
59 16.4 531 2 US-08-928-892-51
58 16.2 374 4 US-09-339-972-51
58 16.2 374 4 US-08-446-100-26
57 15.9 454 3 US-08-446-100-27
57 15.9 454 3 US-08-446-100-28
57 15.9 454 3 US-08-446-100-29
57 15.9 454 3 US-08-446-100-30
57 15.9 454 3 US-08-446-100-30
56.5 15.7 322 4 US-09-134-001C-5120
56.5 15.7 707 4 US-09-328-352-4834
56 15.6 290 4 US-09-252-991A-20895
56 15.6 602 2 US-08-419-652-6
56 15.6 771 1 US-07-923-976-6
56 15.6 783 6 5422248-2

ALIGNMENTS

RESULT 1
US-08-838-151A-44
; Sequence 44, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-44

Query Match 59.3%; Score 213; DB 3; Length 353;

Best Local Similarity 58.6%; Pred. No. 7, 9e-21;

Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLWGEFQVDSARGGCQTSDNDAAEALNASSKEALQIREKIPKYLQFHNLSAL 60

```

Db      110 TIWGGFQVDRSGRGCGCTSDAAAEALNASSKEBALQIIRKIPKYLQFPHNLSAL 169
Qy      61 AAIFDKTPEP 70
      ||| |||
Db      170 ERIFVKVPEP 179

RESULT 2
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

Query Match      59.3%; Score 213; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 7.9e-21;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy      1 TLVWGFQVDRSGRGCGCTSDAAAEALNASSKEBALQIIRKIPKYLQFPHNLSAL 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      110 TIWGGFQVDRSGRGCGCTSDAAAEALNASSKEBALQIIRKIPKYLQFPHNLSAL 169

Qy      61 AAIFDKTPEP 70
      ||| |||
Db      170 ERIFVKVPEP 179

RESULT 3
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul

```

```

; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-49

Query Match      59.3%; Score 213; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 7.9e-21;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy      1 TLVWGFQVDRSGRGCGCTSDAAAEALNASSKEBALQIIRKIPKYLQFPHNLSAL 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      110 TIWGGFQVDRSGRGCGCTSDAAAEALNASSKEBALQIIRKIPKYLQFPHNLSAL 169

Qy      61 AAIFDKTPEP 70
      ||| |||
Db      170 ERIFVKVPEP 179

RESULT 4
US-08-838-151A-52
; Sequence 52, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-52

Query Match 59.3%; Score 213; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 7.9e-21;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSARGCGCOTSDAAEALNASSKEALQIIRKIPKYLQFHNLSAL 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TIWGFQVDRSARGCGQSANDSYAKALNADSIESTLTKKEQPKDYVLQHNIRSL 169

QY 61 AAIFFDKTPEP 70
   |||:|||||
Db 170 ERIFVKVPEP 179

RESULT 5
US-08-838-151A-55
; Sequence 55, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; PRIOR APPLICATION NUMBER:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```

```
;
; MOLECULE TYPE: protein
; US-08-838-151A-55

Query Match 59.3%; Score 213; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 7.9e-21;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSARGCGCOTSDAAEALNASSKEALQIIRKIPKYLQFHNLSAL 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TIWGFQVDRSARGCGQSANDSYAKALNADSIESTLTKKEQPKDYVLQHNIRSL 169

QY 61 AAIFFDKTPEP 70
   |||:|||||
Db 170 ERIFVKVPEP 179

RESULT 6
US-08-809-103B-2
; Sequence 2, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELETYPE: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-2

Query Match 58.8%; Score 211; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.5e-20;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGFQVDRSARGCGCOTSDAAEALNASSKEALQIIRKIPKYLQFHNLSALA 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 LEWGFQVDRSARGCGQTANDAYAKAINAGSKQALDVIKELAPRDYVLQHNIRSL 170

QY 62 AAIFFDKTPEP 70
   |||:|||||
```

Db 171 KVFQVPPAP 179

RESULT 7

US-08-809-103B-4
 ; Sequence 4, Application US/08809103B
 ; Patent No. 6133505
 ; GENERAL INFORMATION:
 ; APPLICANT: GRONENBORN, Bruno
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: YOUNG & THOMPSON
 ; STREET: 745 South 23rd Street
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/809,103B
 ; FILING DATE: 17-MAR-1997
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 94.11040
 ; FILING DATE: 15-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/FR95/01192
 ; FILING DATE: 15-SEP-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PATCH, Andrew J.
 ; REGISTRATION NUMBER: 32,925
 ; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 521-2297
 ; TELEFAX: (703) 685-0573
 ; TELEX: 248425 EMBON
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 359 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-809-103B-4

Query Match 58.8%; Score 211; DB 3; Length 359;

Best Local Similarity 56.5%; Pred. No. 1.5e-20;
 Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRGARGCQTSNDAAALNASKEALQIREKIPKYLFPQHNLNSALA 61
 Db 111 LEWGTQIDGRSARGGQQTANDAYAKAINAGSKQALDVIKELAPRDYVLHFNINSNLD 170

QY 62 AIFDKTPEP 70

Db 171 KVFQVPPAP 179

RESULT 8

US-08-809-103B-6
 ; Sequence 6, Application US/08809103B
 ; Patent No. 6133505
 ; GENERAL INFORMATION:
 ; APPLICANT: GRONENBORN, Bruno
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: YOUNG & THOMPSON
 STREET: 745 South 23rd Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/809,103B
 FILING DATE: 17-MAR-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 94.11040
 FILING DATE: 15-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/FR95/01192
 FILING DATE: 15-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: PATCH, Andrew J.
 REGISTRATION NUMBER: 32,925
 REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 521-2297
 TELEFAX: (703) 685-0573
 TELEX: 248425 EMBON
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-809-103B-6

Query Match 58.8%; Score 211; DB 3; Length 359;

Best Local Similarity 56.5%; Pred. No. 1.5e-20;
 Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRGARGCQTSNDAAALNASKEALQIREKIPKYLFPQHNLNSALA 61
 Db 111 LEWGTQIDGRSARGGQQTANDAYAKAINAGSKQALDVIKELAPRDYVLHFNINSNLD 170

QY 62 AIFDKTPEP 70

Db 171 KVFQVPPAP 179

RESULT 9

US-08-809-103B-8
 ; Sequence 8, Application US/08809103B
 ; Patent No. 6133505
 ; GENERAL INFORMATION:
 ; APPLICANT: GRONENBORN, Bruno
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: YOUNG & THOMPSON
 ; STREET: 745 South 23rd Street
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/809,103B

```
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8

Query Match 58.8%; Score 211; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.5e-20;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGFEQVDSRGSGGQTSNDAAALNASSKEEALQIIREKIPKYLFPQHNLSALA 61
Db 111 LWTGDFQIDGRSARGGQQTANDAYAKAINAGSKQALDVIKELAPRDYVLHFNINSLD 170

QY 62 AIFDKTPEP 70
Db 171 KVFOVPPAP 179

RESULT 10
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match 58.8%; Score 211; DB 3; Length 361;
Best Local Similarity 55.7%; Pred. No. 1.5e-20;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;
```

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-2

Query Match 58.8%; Score 211; DB 3; Length 361;
Best Local Similarity 55.7%; Pred. No. 1.5e-20;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGGQTSNDAAALNASSKEEALQIIREKIPKYLFPQHNLSAL 60
Db 110 TIWGDQFIDGRSARGGQQTANDAYAKAINAGSKQALDVILREBPQKDFVLQNHINSL 169

QY 61 AIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 11
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match 58.8%; Score 211; DB 3; Length 361;
Best Local Similarity 55.7%; Pred. No. 1.5e-20;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGGQTSNDAAALNASSKEEALQIIREKIPKYLFPQHNLSAL 60
Db 110 TIWGDQFIDGRSARGGQQTANDAYAKAINAGSKQALDVILREBPQKDFVLQNHINSL 169
```


; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-24

Query Match 53.8%; Score 193; DB 3; Length 357;
Best Local Similarity 62.3%; Pred. No. 4.3e-18;
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 4 WGEFQVDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSALAAI 63
Db 111 FGVSQIDGRSARGGQSQSANDAYAEALNSGSKSEALNLKEKAPKDYILOFHNLSNLDRI 170
QY 64 F 64
Db 171 F 171

RESULT 15
US-08-838-151A-27
; Sequence 27, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-27

Query Match 53.8%; Score 193; DB 3; Length 357;
Best Local Similarity 62.3%; Pred. No. 4.3e-18;
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
QY 4 WGEFQVDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSALAAI 63
Db 111 FGVSQIDGRSARGGQSQSANDAYAEALNSGSKSEALNLKEKAPKDYILOFHNLSNLDRI 170
QY 64 F 64
Db 171 F 171

Search completed: December 23, 2003, 08:59:35
Job time : 12.6667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

QM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds
(without alignments)

172.015 Million cell updates/sec

Title: US-09-289-346B-7

Perfect score: 359

Sequence: 1 TLVWGFQVDSARGGCQT.....FOFHNLNLSALAIKFTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	359	100.0	70	10	US-09-289-346A-7	Sequence 7, Appli
2	342	95.3	70	10	US-09-289-346A-1	Sequence 1, Appli
3	342	95.3	356	10	US-09-289-346A-11	Sequence 11, Appl
4	334	93.0	70	10	US-09-289-346A-9	Sequence 9, Appli
5	331	92.2	70	10	US-09-289-346A-12	Sequence 12, Appl
6	330	91.9	70	10	US-09-289-346A-16	Sequence 16, Appl
7	328	91.4	70	10	US-09-289-346A-8	Sequence 8, Appli
8	328	91.4	70	10	US-09-289-346A-14	Sequence 14, Appl
9	327	91.1	70	10	US-09-289-346A-2	Sequence 2, Appli
10	327	91.1	70	10	US-09-289-346A-10	Sequence 10, Appl
11	326	90.8	70	10	US-09-289-346A-13	Sequence 13, Appl
12	324	90.3	70	10	US-09-289-346A-4	Sequence 4, Appli
13	324	90.3	70	10	US-09-289-346A-15	Sequence 15, Appl
14	321	89.4	70	10	US-09-289-346A-5	Sequence 5, Appli
15	318	88.6	70	10	US-09-289-346A-6	Sequence 6, Appli

16	86.4	70	10	US-09-289-346A-3	Sequence 3, Appli
17	68	447	9	US-09-989-722-369	Sequence 369, App
18	68	18.9	447	US-09-989-723-369	Sequence 369, App
19	68	18.9	447	US-09-989-279-369	Sequence 369, App
20	68	18.9	447	US-09-989-727-369	Sequence 369, App
21	68	18.9	447	US-09-989-731-369	Sequence 369, App
22	68	18.9	447	US-09-989-732-369	Sequence 369, App
23	68	18.9	447	US-09-991-073-369	Sequence 369, App
24	68	18.9	447	US-09-990-442-369	Sequence 369, App
25	68	18.9	447	US-09-991-163-369	Sequence 369, App
26	68	18.9	447	US-09-993-604-369	Sequence 369, App
27	68	18.9	447	US-09-990-456-369	Sequence 369, App
28	68	18.9	447	US-09-989-721-369	Sequence 369, App
29	68	18.9	447	US-09-992-598-369	Sequence 369, App
30	68	18.9	447	US-09-989-293A-369	Sequence 369, App
31	68	18.9	447	US-09-989-735-369	Sequence 369, App
32	68	18.9	447	US-09-990-444-369	Sequence 369, App
33	68	18.9	447	US-09-991-181-369	Sequence 369, App
34	68	18.9	447	US-09-989-730-369	Sequence 369, App
35	68	18.9	447	US-09-990-436-369	Sequence 369, App
36	68	18.9	447	US-09-993-687-369	Sequence 369, App
37	68	18.9	447	US-09-989-734-369	Sequence 369, App
38	68	18.9	447	US-09-997-653-369	Sequence 369, App
39	68	18.9	447	US-09-993-667-369	Sequence 369, App
40	68	18.9	447	US-09-997-428-369	Sequence 369, App
41	68	18.9	447	US-09-997-666-369	Sequence 369, App
42	68	18.9	447	US-09-990-438-369	Sequence 369, App
43	68	18.9	447	US-09-990-562-369	Sequence 369, App
44	68	18.9	447	US-09-990-711-369	Sequence 369, App
45	68	18.9	447	US-09-984-271-128	Sequence 128, App

ALIGNMENTS

RESULT 1

US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Grullessen, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 60/125,004
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (59)...(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDRI72->ALAA172).
US-09-289-346A-7

Query Match	100.0%	Score 359;	DB 10;	Length 70;
Best Local Similarity	100.0%	Pred. No. 1.7e-33;		
Matches	70;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
QY	1	TLVWGFQVDSARGGCQTNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSAL	60	
Db	1	TLVWGFQVDSARGGCQTNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSAL	60	
QY	61	AAIFDKTPEP	70	

110 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 169

```
Db      61 AAIFDKTPEP 70
|||||
110 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 169

RESULT 2
US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1

Query Match      95.3%; Score 342; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 2.9e-37;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSAL 60
|||||
1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60

Db      61 AAIFDKTPEP 70
|||||
1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60

QY      61 AAIFDKTPEP 70
|||||
1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60

Db      61 DRIFDKTPEP 70
|||||
1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60

RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match      95.3%; Score 342; DB 10; Length 356;
Best Local Similarity 95.7%; Pred. No. 2.5e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSAL 60
|||||
1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
```

```
Db      61 AAIFDKTPEP 70
|||||
110 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 169

RESULT 4
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match      93.0%; Score 334; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 3.3e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSAL 60
|||||
1 TLVWGEFQVAGRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60

Db      61 AAIFDKTPEP 70
|||||
1 TLVWGEFQVAGRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60

QY      61 DRIFDKTPEP 70
|||||
1 TLVWGEFQVAGRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60

RESULT 5
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12

Query Match      92.2%; Score 331; DB 10; Length 70;
```

	Best Local Similarity	92.9%;	Pred. No.	8.2e-36;	
Matches	65;	Conservative	0;	Mismatches	5; Indels 0; Gaps 0;
QY	1 TLVWGEFVDGRSARGGCQTNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSAL	60			
Db	1 TLVWGEFVDGRSARGGCQAASNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSL	60			
QY	61 AAIFDKTPEP 70				
Db	61 DRIFDKTPEP 70				
RESULT 6					
US-09-289-346A-16					
; Sequence 16, Application US/09289346A					
; Patent No. US20020138867A1					
; GENERAL INFORMATION:					
; APPLICANT: Hanley-Bowdoin, Linda					
; APPLICANT: Orozco, Beverly M.					
; APPLICANT: Kong, Ling-Jie					
; APPLICANT: Gruijssem, Wilhelm					
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS					
; FILE REFERENCE: Hanley-Bowdoin et al.					
; CURRENT APPLICATION NUMBER: US/09/289,346A					
; CURRENT FILING DATE: 1999-04-09					
; PRIOR APPLICATION NUMBER: 60/125,004					
; PRIOR FILING DATE: 1999-03-18					
; NUMBER OF SEQ ID NOS: 16					
; SOFTWARE: Patentin Ver. 2.1					
; SEQ ID NO 16					
; LENGTH: 70					
; TYPE: PRT					
; ORGANISM: Tomato golden mosaic virus					
US-09-289-346A-16					
Query Match					
Best Local Similarity 91.9%; Score 330; DB 10; Length 70;					
Matches	65;	Conservative	0;	Mismatches	5; Indels 0; Gaps 0;
QY	1 TLVWGEFVDGRSARGGCQTNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSAL	60			
Db	1 TLVWGEFVDGRSARGGCQTNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSL	60			
QY	61 AAIFDKTPEP 70				
Db	61 DRIFDKTPEP 70				
RESULT 7					
US-09-289-346A-8					
; Sequence 8, Application US/09289346A					
; Patent No. US20020138867A1					
; GENERAL INFORMATION:					
; APPLICANT: Hanley-Bowdoin, Linda					
; APPLICANT: Orozco, Beverly M.					
; APPLICANT: Kong, Ling-Jie					
; APPLICANT: Gruijssem, Wilhelm					
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS					
; FILE REFERENCE: Hanley-Bowdoin et al.					
; CURRENT APPLICATION NUMBER: US/09/289,346A					
; CURRENT FILING DATE: 1999-04-09					
; PRIOR APPLICATION NUMBER: 60/125,004					
; PRIOR FILING DATE: 1999-03-18					
; NUMBER OF SEQ ID NOS: 16					
; SOFTWARE: Patentin Ver. 2.1					
; SEQ ID NO 8					
; LENGTH: 70					
; TYPE: PRT					
; ORGANISM: Tomato golden mosaic virus					
; FEATURE: VARIANT					
; NAME/KEY: (7)..(8)					
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of					

```
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
US-09-289-346A-2

Query Match          91.1%; Score 327; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 2.7e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLSAL 60
   |||||
Db 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60

QY 61 AAIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAAL136->LLLL136).
US-09-289-346A-10

Query Match          91.1%; Score 327; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 2.7e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLSAL 60
   |||||
Db 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60

QY 61 AAIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
```

```
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-13

Query Match          90.8%; Score 326; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 3.7e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLSAL 60
   |||||
Db 1 TLVWGEFQVDRSARGGCGTSDAAAAAEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60

QY 61 AAIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (42)..(44)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAA154).
US-09-289-346A-4

Query Match          90.3%; Score 324; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 6.8e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLSAL 60
   |||||
Db 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIRKIPKYLQFPHNLSNL 60

QY 61 AAIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; FILE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; TITLE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match      90.3%; Score 324; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 6.8e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
Db 1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSAAALQIIREKIPEKYLQFHNLSNL 60

Qy 61 AAIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 14
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; FILE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; TITLE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (EKYL159->AAAL159).
US-09-289-346A-5

Query Match      89.4%; Score 321; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.7e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
Db 1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPAAALQFHNLSNL 60

Qy 61 AAIFDKTPEP 70
Db 61 DRIFDKTPEP 70

```

```

RESULT 15
US-09-289-346A-6
; Sequence 6, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; FILE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; TITLE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (52)..(55)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (QFHN165->AFAA165).
US-09-289-346A-6

Query Match      88.6%; Score 318; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 4.1e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
Db 1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Qy 61 AAIFDKTPEP 70
Db 61 DRIFDKTPEP 70

Search completed: December 23, 2003, 09:43:30
Job time : 76 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds
(without alignments)
673.181 Million cell updates/sec

Title: US-09-289-346B-7
Perfect score: 359
Sequence: 1 TLVWGEFQVGRSARGCQT.....FQFHNLNSALAAIFDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	342	95.3	352	1 QOCVLI	Al1 protein - toma
2	242	67.4	361	1 QOCVTF	Al1 protein - pota
3	229	63.8	358	2 S07594	hypothetical prote
4	222	61.8	362	1 JQ1887	Al1 protein - toma
5	216	60.2	349	2 JQ2300	replicase - pepp
6	216	60.2	349	2 S31875	Al1 protein - pepp
7	215	59.9	359	2 S39211	gene C1 protein -
8	212	59.1	385	2 S28360	Al1 protein - beet
9	211	58.8	359	2 S22593	hypothetical prote
10	210	58.5	355	1 QOCVLI	AVI protein - abut
11	207	57.7	358	1 JQ1870	Al1 protein - toma
12	205	57.1	351	2 JQ2327	Al1 protein - indi
13	205	57.1	359	2 S39235	gene C1 protein -
14	195	54.3	360	2 S59885	replication-associ
15	193	53.8	357	1 QOCVCI	Al1 protein - toma
16	120	33.4	131	2 S45059	AC1 protein (clone
17	107	29.8	347	1 QOCVSI	Al1 protein - squa
18	70	19.5	587	2 JCI419	PC gamma (IgG) rec
19	68	18.9	447	2 T12544	hypothetical prote
20	64.5	18.0	491	2 A81836	leucine aminopepti
21	64	17.8	316	2 C82085	conserved hypotet
22	64	17.8	340	2 B97011	probably O-sialogl
23	63.5	17.7	1229	2 T48959	kinesin-like prote
24	63.5	17.7	1610	2 A46227	voltage-dependent
25	63.5	17.7	1646	2 JH0422	calcium channel al
26	63.5	17.7	2161	2 JH0564	calcium channel al
27	63.5	17.7	2181	2 A38198	voltage-dependent
28	63.5	17.7	2203	2 T42742	protein-Npi-phosph
29	62	17.3	154	2 AD3475	

30 62 17.3 245 2 S76632
31 62 17.3 714 2 C95382
32 61 17.0 1502 1 RGBYH1
33 60.5 16.9 276 2 AC2341
34 60.5 16.9 840 2 T36175
35 59.5 16.6 208 2 E97702
36 59.5 16.6 224 2 I40474
37 59.5 16.6 408 2 A99238
38 59.5 16.6 446 1 S17553
39 59 16.4 338 2 AG3582
40 59 16.4 345 2 AD3024
41 59 16.4 359 2 E98260
42 59 16.4 370 2 T34050
43 59 16.4 384 1 W2WL41
44 59 16.4 2459 2 AF2136
45 58.5 16.3 136 2 T22240

ALIGNMENTS

RESULT 1

QOCVLI
Al1 protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994
C:Accession: A04170
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
A:Residues: 1-352 <HAM>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A

C:Genetics:

A:Map position: segment A

C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 95.3%; Score 342; DB 1; Length 352;
Best Local Similarity 95.7%; Pred. No. 2.5e-31;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGEFQVGRSARGCQTSNDAAALNASSKEALQIIREKIPKYLQFHNLNSAL 60
DB 111 TLVWGEFQVGRSARGCQTSNDAAALNASSKEALQIIREKIPKYLQFHNLNSNL 170
QY 61 AAIFDKTPEP 70
DB 171 DRIFDKTPEP 180

RESULT 2

QOCVTF

Al1 protein - potato yellow mosaic virus (isolate Venezuela)

C:Species: potato yellow mosaic virus

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000

C:Accession: J00364

R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.

J. Gen. Virol. 72, 1515-1520, 1991

A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel

A:Reference number: J00362; MUID:91311403; PMID:1856690

A:Accession: J00364

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-361 <COU>

A:Cross-references: GB:D00940; NID:g222458; PIDN:BAA00782.1; PID:g222459

C:Genetics:

A:Map position: segment A

C:Superfamily: tomato golden mosaic virus Al1 protein

submitted to the EMBL Data Library, August 1993

A;Description: High similarity among the tomato yellow leaf curl virus isolates from the submitted to the EMBL Data Library, August 1993

J02327
 A1: protein - Indian caseava mosaic virus
 N: Alternate names: replication-associated protein
 C: Species: Indian caseava mosaic virus
 C: Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 20-Sep-1999
 C: Accession: J02327; S59883
 R: Hong, Y.G.; Robinson, D.J.; Harrison, B.D.
 J. Gen. Virol. 74, 2437-2443, 1993
 A: Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-transmitted geminiviruses
 A: Reference number: J02326; MUID:94065670; PMID:8245859
 A: Accession: J02327
 A: Molecule type: DNA
 A: Residues: 1-351 <NON>
 A: Cross-references: EMBL:224758; NID:9395351; PIDN:CAA80891.1; PID:9584046
 C: Superfamily: tomato golden mosaic virus A11 protein

Query Match 57.1%; Score 205; DB 2; Length 351;
 Best Local Similarity 59.7%; Pred. No. 1.1e-15;
 Matches 40; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 4 WGEFQVDSARGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSALAAI 63
 DB 113 WGTFTQIDGRSARGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSALAAI 172

QY 64 FDKTPEP 70
 DB 173 FTKPPPP 179

RESULT 13
 S39235
 gene C1 protein - tomato yellow leaf curl virus
 C: Species: tomato yellow leaf curl virus
 C: Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
 C: Accession: S39235
 R: Crespi, S.; Noris, E.; Vaira, A.; Bosco, D.; Accotto, G.
 submitted to the EMBL Data Library, December 1993
 A: Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.
 A: Reference number: S39233
 A: Accession: S39235
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-359 <CRE>
 A: Cross-references: EMBL:228390; NID:gl041671; PID:gl334964
 C: Superfamily: tomato golden mosaic virus A11 protein

Query Match 57.1%; Score 205; DB 2; Length 359;
 Best Local Similarity 55.1%; Pred. No. 1.1e-15;
 Matches 38; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 2 LWGEFQVDSARGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSALA 61
 DB 111 LEWGTFTQIDGRSARGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSALD 170

QY 62 AFDKTPPEP 70
 DB 171 KYFQVPPAP 179

RESULT 14
 S59885
 replication-associated protein C1 - tomato yellow leaf curl virus
 C: Species: tomato yellow leaf curl virus
 C: Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
 C: Accession: S59885
 R: Hong, Y.; Harrison, B.D.
 submitted to the EMBL Data Library, February 1995
 A: Description: Nucleotide sequences from tomato leaf curl viruses from different countries
 A: Reference number: S58346
 A: Accession: S59885
 A: Status: preliminary
 A: Molecule type: DNA

A: Residues: 1-360 <NON>
 A: Cross-references: EMBL:248182; NID:9344838; PIDN:CAA88229.1; PID:9974211
 C: Superfamily: tomato golden mosaic virus A11 protein

Query Match 54.3%; Score 195; DB 2; Length 360;
 Best Local Similarity 57.6%; Pred. No. 1.6e-14;
 Matches 38; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 4 WGEFQVDSARGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSALAAI 63
 DB 113 FGVFQIDGRSARGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSALDRI 172

QY 64 FDKTPEP 69
 DB 173 FTFSAE 178

RESULT 15
 Q0CVCI
 A11 protein - tomato yellow leaf curl virus
 N: Alternate names: C1 protein
 C: Species: tomato yellow leaf curl virus
 C: Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
 C: Accession: D40779
 R: Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.
 Virology 185, 151-161, 1991
 A: Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single
 A: Reference number: A40779; MUID:92024070; PMID:1926771
 A: Accession: D40779
 A: Status: translation not shown
 A: Molecule type: DNA
 A: Residues: 1-357 <NAV>
 A: Cross-references: GB:X15656; NID:962204; PIDN:CAA33688.1; PID:962207
 C: Superfamily: tomato golden mosaic virus A11 protein

Query Match 53.8%; Score 193; DB 1; Length 357;
 Best Local Similarity 52.3%; Pred. No. 2.7e-14;
 Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 4 WGEFQVDSARGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSALAAI 63
 DB 111 FGVFQIDGRSARGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSALDRI 170

QY 64 F 64
 DB 171 F 171

Search completed: December 23, 2003, 09:05:23
 Job time: 11 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds
(without alignments)
569.747 Million cell updates/sec

Title: US-09-289-346B-7

Perfect score: 359

Sequence: 1 TLVWGEFQVDSARGGCQT.....FQHNLSALAAIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	342	95.3	352	1 VAL1_TGMV	P03567 tomato gold
2	242	67.4	361	1 VAL1_PYMV	P27258 potato yell
3	229	63.8	358	1 VAL1_CLVK	P14982 cassava lat
4	229	63.8	358	1 VAL1_CLVN	P14972 cassava lat
5	222	61.8	362	1 VAL1_TYLC	P36279 tomato yell
6	216	60.2	349	1 VAL1_PHVU	Q06923 pepper huas
7	215	59.9	359	1 VAL1_TYLCU	P38609 tomato yell
8	212	59.1	358	1 VAL1_BCTV	P14991 beet curly
9	211	58.8	353	1 VAL1_BGMV	P05175 bean golden
10	211	58.8	359	1 VAL1_TYLCM	P27260 tomato yell
11	210	58.5	355	1 VAL1_ABMVW	P21947 abutilon no
12	207	57.7	361	1 VAL1_TMOV	Q06857 tomato mott
13	193	53.8	357	1 VAL1_TYLCV	P27259 tomato yell
14	107	29.8	347	1 VAL1_SLUCV	P29048 squash leaf
15	68	18.9	447	1 TBL2_HUMAN	Q9Y4P3 homo sapien
16	65.5	18.2	298	1 OLIG2_CHICK	Q90XB3 gallus gall
17	64.5	18.0	491	1 AMPA_ANASP	Q82064 anabaena sp
18	63.5	17.7	1610	1 CCAD_MESAU	Q99244 mesocricetu
19	63.5	17.7	2161	1 CCAD_HUMAN	Q01568 homo sapien
20	63.5	17.7	2203	1 CCAD_RAT	P27732 rattus norv
21	61.5	17.1	476	1 DGRE_HUMAN	Q96df8 homo sapien
22	61.5	17.1	479	1 DGRE_MOUSE	P07279 mus musculu
23	61	17.0	1502	1 CYP1_YEAS	P12351 saccharomyc
24	59.5	16.6	224	1 SP2R_BACSU	P39151 bacillus su
25	59.5	16.6	4466	1 DYHC_TRIGR	P23098 tripeustes
26	59	16.4	370	1 CC37_CABEL	Q02108 caenorhabdi
27	59	16.4	387	1 VE2_HPV41	P27552 human papil
28	59	16.4	387	1 Y4PF_RHISN	P55615 rhizobium s
29	58.5	16.3	136	1 Y452_CABEL	Q62250 caenorhabdi
30	58.5	16.3	299	1 Y175_HELPJ	Q9ZMQ7 helicobacte
31	57.5	16.0	367	1 LHX4_MOUSE	P53776 mus musculu
32	57.5	16.0	1852	1 CCAS_CYPCA	P22316 cyprinus ca
33	57	15.9	247	1 YCP4_YEAST	P25349 saccharomyc

34 57 15.9 256 1 UT11_YEAST P34247 saccharomyc
35 56.5 15.7 511 1 HUTH_VIBCH Q9K9Q4 vibrio chol
36 56.5 15.7 2190 1 CCAD_CHICK Q73700 gallus gall
37 56 15.6 98 1 VATF_METJA Q57671 methanococc
38 56 15.6 295 1 VAL1_CSNV P18921 chloris str
39 56 15.6 295 1 VAL1_TYDVA P31617 tobacco yel
40 56 15.6 492 1 MOT3_MOUSE P35308 mus musculu
41 56 15.6 492 1 MOT3_RAT Q70461 rattus norv
42 56 15.6 836 1 CCSR_HUMAN Q99662 homo sapien
43 55.5 15.5 266 1 ETFB_MYCTU Q33095 mycobacteri
44 55.5 15.5 266 1 ETFB_MYCTU Q53276 mycobacteri
45 55.5 15.5 428 1 GBA1_CANAL P28868 candida alb

ALIGNMENTS

RESULT 1
VAL1_TGMV STANDARD; PRT; 352 AA.
ID VAL1_TGMV
AC P03567;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Tomato golden mosaic virus (TGMV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI TaxID=10831;
RN [1]_TAXID=10831;
SEQUENCE FROM N.A.
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;
RT "Complete nucleotide sequence of the infectious cloned DNA components
of tomato golden mosaic virus: potential coding regions and regulatory
sequences.";
RL EMBO J. 3:2197-2205 (1984).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.ebi.ac.uk/announcements/
or send an email to license@ebi.ac.uk).

EMBL; K02029; -; NOT ANNOTATED CDS.
PIR; A04170; QQCVL1.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOAT1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 223 230
SQ SEQUENCE 352 AA; 40332 MW; C33C938E9644B4A4 CRC64;

Query Match 95.3%; Score 342; DB 1; Length 352;
Best Local Similarity 95.7%; Pred. No. 4.9e-32;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCQTNDAAAEALNASSKEALQIREKIPEKYLQFHNLSAL 60
DB 111 TLVWGEFQVDSARGGCQTNDAAAEALNASSKEALQIREKIPEKYLQFHNLSAL 170
QY 61 AAIFDKTPEP 70
DB 171 DRIFDKTPEP 180

RESULT 2

VAL1_PYMV
ID VAL1_PYMV STANDARD; PRT; 361 AA.
AC P27258;

```

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A.; Coffin R.S.; Roberts E.J.P.; Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520 (1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D00940; BAA00782.1; -
CC PIR; J0364; CQCVP.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
CC NP BIND 222 229 ATP (POTENTIAL).
CC SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;
CC -----
Query Match 67.4%; Score 242; DB 1; Length 361;
Best Local Similarity 66.9%; Pred. No. 1.8e-20; Indels 0; Gaps 0;
Matches 46; Conservative 11; Mismatches 12;
CC -----
QY 1 TLVWGFQVDGRSARGCGQTNDAAALNASKEALQIREKIPKYLQFHNLSAL 60
DB 110 TLVWGFQVDGRSARGCGQTNDAAALNASKEALQIREKIPKYLQFHNLSAL 169
QY 61 AAIFDKTPE 69
DB 170 DRIFDKAPE 178
CC -----
RESULT 3
VAL1 CLVK
ID VAL1 CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX Stanley J.; Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA."
RL Nature 301:260-262 (1993).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----

```

```

CC EMBL; J02057; -; NOT ANNOTATED CDS.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
CC NP BIND 220 227 ATP (POTENTIAL).
CC SEQUENCE 358 AA; 40346 MW; ED173E753EE92D69 CRC64;
CC -----
Query Match 63.8%; Score 229; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 5.5e-19;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
CC -----
QY 1 TLVWGFQVDGRSARGCGQTNDAAALNASKEALQIREKIPKYLQFHNLSAL 60
DB 109 TLVWGFQVDGRSARGCGQTNDAAALNASKEALQIREKIPKYLQFHNLSAL 169
QY 61 AAIFDKTPE 70
DB 169 DRIFQEPAP 178
CC -----
RESULT 4
VAL1 CLVN
ID VAL1 CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B.; Coates L.; Lowe S.; Richardson K.; Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain)."
RL Nucleic Acids Res 18:197-198 (1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X17095; CAA34953.1; -
CC PIR; S07594; S07594.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
CC NP BIND 220 227 ATP (POTENTIAL).
CC SEQUENCE 358 AA; 40435 MW; 1DB16BB0CE2D5E2C CRC64;
CC -----
Query Match 63.8%; Score 229; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 5.5e-19;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
CC -----
QY 1 TLVWGFQVDGRSARGCGQTNDAAALNASKEALQIREKIPKYLQFHNLSAL 60
DB 109 TLVWGFQVDGRSARGCGQTNDAAALNASKEALQIREKIPKYLQFHNLSAL 168
QY 61 AAIFDKTPE 70
DB 169 DRIFQEPAP 178

```

```

RESULT 5
VAL1 TYLCA STANDARD; PRT; 362 AA.
ID VAL1 TYLCA STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Rigden J.E., Krake L.R., Mullineux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
geminivirus.";
RL J. Gen. Virol. 74:147-151(1993).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR PIR; JQ1887; JQ1887.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 61.8%; Score 222; DB 1; Length 362;
Best Local Similarity 52.9%; Pred. No. 3.6e-18;
Matches 45; Conservative 9; Mismatches 15; Indels 16; Gaps 1;

Qy 1 TLWGFQVQDGRSARGCGQTSNDAAAEALNASKEALQIREKIPEKYLFOFHNLSAL 60
Db 110 TLEWGFQVQDGRSARGCGQTSNDAAAEALNASKEALQIREKIPEKYLFOFHNLSAL 169

Qy 61 AAI-----FDKTPPE 69
Db 170 DRIFTPPLEVYVFFLSSSFDVPE 194

RESULT 6
VAL1 PHUV STANDARD; PRT; 349 AA.
ID VAL1 PHUV STANDARD; PRT; 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AL1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
comparison with bipartite geminiviruses.";
RL J. Gen. Virol. 74:2225-2231(1993).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

Query Match 59.9%; Score 215; DB 1; Length 359;
Best Local Similarity 58.0%; Pred. No. 2.3e-17;
Matches 40; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

Qy 2 LVWGFQVQDGRSARGCGQTSNDAAAEALNASKEALQIREKIPEKYLFOFHNLSALA 61
Db 111 LEWGTFTQDGRSARGCGQTSNDAAAEALNASKEALQIREKIPEKYLFOFHNLSNLD 170

```

```

QY      62 AIFDKTPEP 70
Db      171 RVFQVPPAP 179

RESULT 8
VAL1_BCTV STANDARD; PRT; 358 AA.
AC P14931;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
RT beet curly top virus."
RL EMBO J. 5:1761-1767(1986).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M10070; AAA46318.1; .
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATAL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding. 222 229 ATP (POTENTIAL).
FT NP BIND 222 229
SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 59.1%; Score 212; DB 1; Length 358;
Best Local Similarity 55.7%; Pred. No. 5.1e-17;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY      1 TLVWGFQVDSARGGQTSNDAAAEALNASSKEEALQIREKIPKYLQFHNLSAL 60
Db      110 TIEWGFQVDSARGGQTSNDAAAEALNASSKEEALQIREKIPKYLQFHNLSAL 169
QY      61 AALFDKTPPEP 70
Db      170 QKIFQRPDP 179

RESULT 10
VAL1_TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (C1 protein).
DE AL1 protein (C1 protein).
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RA Khayat-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a
RT whitefly-transmitted monopartite geminivirus."
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X61153; CAA43466.1; .
DR PIR; S22593; S22593.
DR PDB; 1L2M; 18-SEP-02.
DR PDB; 1L5I; 18-SEP-02.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATAL1.
DR ProDom; PD000736; Gemini AL1; 1.
KW ATP-binding; 3D-structure.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 40733 MW; 9717BAA07C93EFA7 CRC64;

```

Query Match 59.8%; Score 211; DB 1; Length 359;
 Best Local Similarity 56.5%; Pred. No. 6.6e-17;
 Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LWGFEQVDSARGGCGTSDNDAAEALNASSKEALQIIREKIPKYLQFPHNLSAL 61
 DB 111 LEWGTQIDGSRGCGTANDAYAKAINAGSQALDVIKELAPRDYVLHFNHNSLD 170

QY 62 AIFDKTPEP 70

DB 171 KVFQVPPAP 179

RESULT 11

ID VAL1 ABMVW STANDARD; PRT; 355 AA.
 AC P21947;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE AL1 protein.

GN AC1.
 OS Abutilon mosaic virus (isolate West India).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10816;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91020984; PubMed=2219703;
 RA Frischmuth T., Zimmatt G., Jeske H.;
 RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
 as well as eukaryotic features."
 RL Virology 178:461-468(1990).

CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL; X15983; -; NOT_ANNOTATED_CDS.
 DR PIR; A36214; OQCVW1.
 DR InterPro; IPR001191; Gemini_AL1.
 DR Pfam; PF00799; Gemini_AL1; 1.
 DR PRINTS; PR00227; GEMCOATALL.
 DR ProDom; PD000736; Gemini_AL1; 1.
 KW ATP-binding.

FT NP BIND 221 228 ATP (POTENTIAL).
 SQ SEQUENCE 355 AA; 40257 MW; 16A2CA8A63251E95 CRC64;
 Query Match 58.5%; Score 210; DB 1; Length 355;
 Best Local Similarity 57.1%; Pred. No. 8.5e-17;
 Matches 40; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1 TLWGEFQVDSARGGCGTSDNDAAEALNASSKEALQIIREKIPKYLQFPHNLSAL 60
 DB 110 TRWGEFQVDSARGGCGTANDAYAKAINAGSQALDVQSNALILKEBPQKDYVLQHNIRSNL 169

QY 61 AAFDKTPEP 70

DB 170 ERIFAKAPEP 179

RESULT 12

ID VAL1 TMOV STANDARD; PRT; 361 AA.
 AC Q06657;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE AL1 protein.

GN AL1.
 OS Tomato mottle virus (isolate Florida) (TMov).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=36449;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9107858; PubMed=1469361;
 RA Abouzid A.M., Polson J.E., Hiebert E.;
 RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
 isolated from tomatoes in Florida."
 RL J. Gen. Virol. 73:3225-3229(1992).

CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL; L14460; AAC32414.1; -.

DR PIR; JQ1870; JQ1870.

DR InterPro; IPR001191; Gemini_AL1.

DR Pfam; PF00799; Gemini_AL1; 1.

DR PRINTS; PR00227; GEMCOATALL.

DR ProDom; PD000736; Gemini_AL1; 1.

KW ATP-binding.

FT NP BIND 222 229 ATP (BY SIMILARITY).

SQ SEQUENCE 361 AA; 40516 MW; 813BB65CEAC6950 CRC64;

Query Match 57.7%; Score 207; DB 1; Length 361;

Best Local Similarity 54.3%; Pred. No. 1.9e-16;

Matches 38; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLWGEFQVDSARGGCGTSDNDAAEALNASSKEALQIIREKIPKYLQFPHNLSAL 60
 DB 110 TRWGEFQVDSARGGCGTANDAYAKAINAGSQALDVQSNALILKEBPQKDYVLQHNIRSNL 169

QY 61 AAFDKTPEP 70

DB 170 ERIFAKAPEP 179

RESULT 13

ID VAL1 TYLCV STANDARD; PRT; 357 AA.
 AC P27259;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE AL1 protein (C1 protein).

GN C1.

OS Tomato yellow leaf curl virus (TYLCV).

OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

OX NCBI_TaxID=10832;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9204070; PubMed=1926771;

RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;

RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
 with a single genomic component."

RL Virology 185:151-161(1991).

CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC

```

DR EMBL; X15656; CAA33688.1; --
DR F00779; Q0CVCL; Gemini_AL1.
DR InterPro; IPR001131; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
FT NP BIND 219 226 ATP (POTENTIAL).
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match
Best Local Similarity 53.8%; Score 193; DB 1; Length 357;
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 4 WGFQVDSRGSGGQTSNDAAEALNASSKEALQIREKIPEKYLFPFNLNSALAAI 63
Db 111 FGVSDIGRSARGGQSQANDAAEALNASSKEALQIREKIPEKYLFPFNLNSALDRI 170

Qy 64 F 64
Db 171 F 171

RESULT 14
VAL1 SLCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE AL1 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G., Lazdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype.";
RL Virology 180:58-69(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M38183; AAC32410.1; ALT_INIT.
DR PIR; C36785; Q0CVS1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
FT NP BIND 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDAEBDD1221110E CRC64;

Query Match
Best Local Similarity 29.8%; Score 107; DB 1; Length 347;
Matches 23; Conservative 13; Mismatches 26; Indels 4; Gaps 1;

Qy 5 GEFQVDSRGSGGQTSNDAAEALNASSKEALQIREKIPEKYLFPFNLNSALAAIF 64
Db 116 GQYKVSQ---GSKSNKDDVYHNAVNSAGSAGEALDIKAGDKTFYVYNNLLANVERLP 171

Qy 65 DKTPEP 70
Db 172 QKPEP 177

```

```

RESULT 15
TBL2_HUMAN STANDARD; PRT; 447 AA.
ID TBL2_HUMAN
AC Q9Y4P3; Q9OQB2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transducin beta-like 2 protein (WS beta-transducin repeats protein).
DE (WS-betaTRP) (Williams-Beuren syndrome chromosome region 13 protein).
DE TBL2 OR WBSCTR13.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20044626; PubMed=10575226;
RA Perez Jurado L.A., Wang Y.-K., Francke U., Cruces J.;
RT "TBL2, a novel transducin family member in the WBS deletion:
RT characterization of the complete sequence, genomic structure,
RT transcriptional variants and the mouse ortholog.";
RL Cytogenet. Cell Genet. 86:277-284(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansoorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
RA Mewes H.-W., Ottenwaelter B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
RN [3]
RP SEQUENCE OF 14-447 FROM N.A.
RX MEDLINE=99075645; PubMed=9860302;
RA Meng X., Lu X., Li Z., Green E.D., Massa H., Trask B.J., Morris C.A.,
RA Keating M.T.;
RT "Complete physical map of the common deletion region in Williams
RT syndrome and identification and characterization of three novel
RT genes.";
RL Hum. Genet. 103:590-599(1998).
CC -1- DISASE: haploinsufficiency of TBL2 may be the cause of certain
CC cardiovascular and musculo-skeletal abnormalities observed in
CC Williams-Beuren syndrome (WBS) [MIM:194050], a rare developmental
CC disorder. It is a contiguous gene deletion syndrome involving
CC genes from chromosome band 7q11.23.
CC -1- SIMILARITY: Contains 7 WD repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF097484; AAF06823.1; --
DR EMBL; AF097485; AAF06824.1; --
DR EMBL; AL080162; CAB45751.1; --
DR EMBL; AF056183; AAD28083.1; ALT_INIT.
DR PIR; T12544; T12544.
DR Genew; HGNC:11586; TBL2.
DR MIM; 605842; --
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 5.
DR PRINTS; PR00320; GPROTEINRPT.
DR ProDom; PD000018; WD40; 2.
DR SMART; SM00320; WD40; 5.

```


Search completed: December 23, 2003, 08:57:40
Job time : 6.77778 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 25.3333 Seconds
(without alignments)
713.040 Million cell updates/sec

Title: US-09-289-346B-7

Perfect score: 359

Sequence: 1 TLVGEFQVDRGARGCQOT.....FQFHNLNSALAIKFTPEP 70

Scoring table: BLQSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_todent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_virus.*

16: sp_bacteriaph.*

17: sp_archaeap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	293	81.6	351	Q91R10	Q91R10 tomato seve
2	291	81.1	352	Q9E000	Q9E000 tomato rugo
3	283	78.8	232	Q8QPV3	Q8QPV3 tomato chlo
4	274	76.3	226	Q9WHF6	Q9WHF6 tomato mild
5	274	76.3	226	Q09727	Q09727 leonurus mo
6	272	75.8	361	Q67574	Q67574 bean golden
7	270	75.2	225	Q9QDB1	Q9QDB1 cowpea gold
8	270	75.2	314	Q9ELT8	Q9ELT8 sweet potat
9	270	75.2	364	Q9QS55	Q9QS55 sweet potat
10	267	74.4	185	Q98693	Q98693 sida golden
11	263	73.3	235	Q8QPU4	Q8QPU4 tomato infe
12	262	73.0	208	Q8TLV3	Q8TLV3 potato yell
13	262	73.0	289	Q8JLY5	Q8JLY5 potato yell
14	259	72.1	149	P88975	P88975 macroptiliu
15	259	72.1	233	Q9YLA4	Q9YLA4 macroptiliu
16	258	71.9	234	Q39180	Q39180 geminivirid

17	258	71.9	361	12	Q8JMW4	Q8jmw4 potato yell
18	256	71.3	360	12	Q8QWH4	Q8qwh4 sida mottle
19	254	70.8	361	12	Q8QVH0	Q8qvho ageratum en
20	252	70.2	190	12	Q9Z089	Q9z089 tobacco lea
21	252	70.2	190	12	Q9Z084	Q9z084 tobacco lea
22	251	69.9	223	12	Q8QP07	Q8qp07 tobacco seve
23	249	69.4	190	12	Q9W827	Q9w827 tobacco lea
24	249	69.4	208	12	Q9Z0C4	Q9z0c4 tobacco lea
25	249	69.4	353	12	Q72692	Q72692 beet curly
26	249	69.4	354	12	Q65438	Q65438 beet curly
27	249	69.4	359	12	Q91M88	Q91m88 tobacco lea
28	249	69.4	359	12	Q8JVE8	Q8jve8 tomato curl
29	247	68.8	208	12	Q9Z0C0	Q9z0c0 tobacco lea
30	247	68.8	208	12	Q9Z0B8	Q9z0b8 tobacco lea
31	246	68.5	203	12	Q9Z0B6	Q9z0b6 tobacco lea
32	245	68.2	208	12	Q9Z0B6	Q9z0b6 tobacco lea
33	245	68.2	358	12	Q65418	Q65418 beet curly
34	244	68.0	363	12	Q73577	Q73577 cotton leaf
35	239	66.6	359	12	Q91B86	Q91b86 ageratum ye
36	239	66.6	360	12	Q9DX10	Q9dx10 ageratum ye
37	238	66.3	190	12	Q9Z086	Q9z086 tobacco lea
38	238	66.3	248	12	Q91LW5	Q91lw5 macroptiliu
39	238	66.3	362	12	Q56816	Q56816 chayote mos
40	237	66.0	208	12	Q9Z0A0	Q9z0a0 tobacco lea
41	237	66.0	362	12	Q8V016	Q8v016 cotton leaf
42	237	66.0	362	12	Q8V018	Q8v018 cotton leaf
43	237	66.0	362	12	Q8V618	Q8v618 cotton leaf
44	237	66.0	362	12	Q8V0H6	Q8v0h6 okra leaf c
45	237	66.0	362	12	Q9IN48	Q9in48 okra enatio

ALIGNMENTS

RESULT 1

Q91R10 PRELIMINARY; PRT; 351 AA.
AC Q91R10;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Rep protein.
GN ACI.
OS Tomato severe rugose virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_Taxid=158463;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Minas Gerais;
RA Rezende W.L., Goulart L.R., Parreira K.S., Figueiredo J.E.F.;
RT "The full-length DNA-A nucleotide sequence of a novel tomato-infecting begomovirus, Tomato severe rugose virus, in Brazil."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029750; AAK50357.1;
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 351 AA; 40122 MW; 87F937A4F873B6CF CRC64;

Query Match 81.6%; Score 293; DB 12; Length 351;

Best Local Similarity 78.8%; Pred. No. 5.1e-26;

Matches 55; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 TLVGEFQVDRGARGCQOTSDAAALNSAKKEALQIIEKIPKYLQFQHNLSAL 60

Db 111 TIENGEFOIDGRGARGCQOTDAAALNSAKKEALQIIEKIPKYLQFQHNLSNL 170

QY 61 AAIKFTPEP 70

Db 171 DRIFARAPEP 180

110 TLEWGEFQIDGRSARGGQQTNDAAALNASSKEAMQIIRKPKLFQYHNLSSL 169

111 TLEWGEFQIDGRSARGGQQTNDAAALNASSKEAMQIIRKPKLFQYHNLSSL 170

Db QY 61 AAIFDKTPEP 70
170 DRIFSKAPEP 179

RESULT 4
Q9WHF6 PRELIMINARY; PRT; 226 AA.
ID Q9WHF6
AC Q9WHF6
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE Replication-associated protein (fragment).
GN REP.
OS Tomato mild mottle geminivirus.
OC Viruses; ssDNA viruses; Geminiviridae; unclassified Geminiviridae.
OX NCBI_TaxID=92943;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HN96-H5Kw;
RA Nakhla M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M.,
RA Maxwell D.P.;
RT "Molecular characterization and DNA-based detection methods for
RT vegetable-infecting geminiviruses in Central America."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131071; AAD33471.1;
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1.
FT NON_TER 226 226
SQ SEQUENCE 226 AA; 25941 MW; 2EA4116712871A23 CRC64;

Query Match 76.3%; Score 274; DB 12; Length 226;
Best Local Similarity 72.9%; Pred. No. 5.1e-24;
Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGQQTNDAAALNASSKEAMQIIRKPKLFQYHNLSSL 60
111 TLEWGEFQIDGRSARGGQQTNDAAALNASSKEAMQIIRKPKLFQYHNLSSL 170

Db QY 61 AAIFDKTPEP 70
171 DRIFSKAPEP 180

RESULT 5
O09727 PRELIMINARY; PRT; 226 AA.
ID O09727
AC O09727
DT 01-JUL-1997 (TREMELrel. 04, Created)
DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Rep protein (fragment).
GN REP.
OS Leucurus mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=58177;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LeMV- Brazil 1;
RA Faria J.C., Maxwell D.P.;
RT "Variability in geminivirus associated with Phaseolus vulgaris in
RT Brazil."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U92532; AAB51157.1;
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1.
FT NON_TER 226 226

Db QY 61 AAIFDKTPEP 70
171 DRIFSKAPEP 180

RESULT 3
Q8QPV3 PRELIMINARY; PRT; 232 AA.
ID Q8QPV3
AC Q8QPV3
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Replication-associated protein (fragment).
GN AC1.
OS Tomato chlorotic vein virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DF-Bri;
RA Ribeiro S.G., Ambrozovic L.P., de Avila A.C., Calegario R.F.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049205; AAL82824.1;
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.
DR ProDom; PD000736; Gemini_AL1.
FT NON_TER 232 232
SQ SEQUENCE 232 AA; 26319 MW; 254CA5D040D35DDA CRC64;

Query Match 78.8%; Score 283; DB 12; Length 232;
Best Local Similarity 77.1%; Pred. No. 4.7e-25;
Matches 54; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGQQTNDAAALNASSKEAMQIIRKPKLFQYHNLSSL 60
111 TLEWGEFQIDGRSARGGQQTNDAAALNASSKEAMQIIRKPKLFQYHNLSSL 170

SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;
 Query Match 76.3%; Score 274; DB 12; Length 226;
 Best Local Similarity 77.1%; Pred. No. 5.1e-24;
 Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDRSGRGCGTNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSAL 60
 DB 111 TVWGFQVDRSGRGCGTNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 170
 QY 61 AAIFDKTPEP 70
 DB 171 DRIFAKAPEP 180
 RESULT 6
 Q67574 PRELIMINARY; PRT; 361 AA.
 AC Q67574;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE Putative replicative protein.
 GN ALI.
 OS Bean golden mosaic virus.
 OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=10839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
 RA Maxwell D.P., Russell D.R.;
 RA "Cloning of the complete DNA genomes of four bean-infecting
 RT geminiviruses and determining their infectivity by electric discharge
 RT particle acceleration."
 RL Phytopathology 81:980-985(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
 RA Morales F.J., Maxwell D.P.;
 RT "Differentiation of bean-infecting geminiviruses by nucleic acid
 RT hybridization probes and aspects of bean golden mosaic in Brazil."
 RL Plant Dis. 75:336-342(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
 RT "Genetic diversity in geminiviruses causing bean golden mosaic
 RT disease: The nucleotide sequence of the infectious cloned DNA
 RT components of a Brazilian isolate of bean golden mosaic geminivirus."
 RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M88686; AAA46312.1; -;
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; I.
 DR PRINTS: PR00227; GEMCOATL1.
 DR PRODOM: PD000736; Gemini_AL1; 1.
 SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;
 Query Match 75.8%; Score 272; DB 12; Length 361;
 Best Local Similarity 76.1%; Pred. No. 1.5e-23;
 Matches 51; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
 QY 4 WGFQVDRSGRGCGTNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSALAI 63
 DB 113 WGFQVDRSGRGCGTNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNLDRI 172
 QY 64 FDKTPEP 70
 DB 173 FTKAPDP 179
 RESULT 7
 Q9QDB1 PRELIMINARY; PRT; 225 AA.
 ID Q9QDB1
 AC Q9QDB1;

DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE Replication associated protein (Fragment).
 GN REP.
 OS Cowpea golden mosaic virus.
 OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=69263;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=CGMV-BR;
 RA Faria J.C.;
 RA "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
 RT Brazil."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF188708; AAF06318.1; -;
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; I.
 DR PRINTS: PR00227; GEMCOATL1.
 DR PRODOM: PD000736; Gemini_AL1; 1.
 FT NON TER 225 225
 SQ SEQUENCE 225 AA; 25766 MW; 1089CB6BD15B5D CRC64;
 Query Match 75.2%; Score 270; DB 12; Length 225;
 Best Local Similarity 76.1%; Pred. No. 1.5e-23;
 Matches 51; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
 QY 4 WGFQVDRSGRGCGTNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSALAI 63
 DB 113 WGFQVDRSGRGCGTNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNLDRI 172
 QY 64 FDKTPEP 70
 DB 173 FTKAPDP 179
 RESULT 8
 Q9ELT8 PRELIMINARY; PRT; 314 AA.
 ID Q9ELT8
 AC Q9ELT8;
 DT 01-MAR-2001 (TREMELrel. 16, Created)
 DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE Replication associated protein.
 GN ACI.
 OS Sweet potato leaf curl virus.
 OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=100755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
 RT "Detection of a geminivirus infecting sweet potato in the United
 RT States."
 RL Plant Dis. 82:1253-1257(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF288227; AAG01006.1; -;
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; I.
 DR PRINTS: PR00227; GEMCOATL1.
 DR PRODOM: PD000736; Gemini_AL1; 1.
 SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;
 Query Match 75.2%; Score 270; DB 12; Length 314;
 Best Local Similarity 79.4%; Pred. No. 2.2e-23;
 Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
 QY 1 TLVWGFQVDRSGRGCGTNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSAL 60
 DB 110 TLVWGFQVDRSGRGCGTNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 169

```

QY 61 AAIFDKTP 68
DB 170 DRIFSPPP 177

RESULT 9
Q9QS55 PRELIMINARY; PRT; 364 AA.
AC Q9QS55;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl virus; nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-line 0:0-0(1999).
DR EMBL; AF104036; AAD47173.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Geminini_AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 75.2%; Score 270; DB 12; Length 364;
Best Local Similarity 79.4%; Pred. No. 2.7e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSRGSGCQTNDAAAEALNASSKEEALQIIREKIPKYLFOFHNLSAL 60
DB 110 TITWGFQVDSRGSGCQTNDAAAEALNASSKEEALQIIREKIPKYLFOFHNLSAL 169
QY 61 AAIFDKTP 68
DB 170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica;
RC STRAIN=Jamaica;
RA Roye M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RT "Genetic Diversity among Geminiviruses associated with the weed species Sida spp., Macroptilium lathyroides, and Wissadula amplissima from Jamaica.";
RL Plant Dis. 81:1251-1258(1997).
DR EMBL; U67926; AAB97865.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.

QY 61 AAIFDKTP 68
DB 170 DRIFSPPP 177

RESULT 11
Q8QPU4 PRELIMINARY; PRT; 235 AA.
AC Q8QPU4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RA Ribeiro S.G., Ambrozevicus L.P., de Avila A.C., Calegario R.P.,
RT "Distribution and genetic diversity of tomato-infecting geminiviruses in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049208; AAL82833.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR ProDom; PD000736; Geminini_AL1; 1.
FT NON TER 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BE0DD9C810 CRC64;

Query Match 73.3%; Score 263; DB 12; Length 235;
Best Local Similarity 73.1%; Pred. No. 1e-22;
Matches 49; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 4 WGEFQVDSRGSGCQTNDAAAEALNASSKEEALQIIREKIPKYLFOFHNLSAL 63
DB 113 WGFQVDSRGSGCQTNDAAAEALNASSKEEALQIIREKIPKYLFOFHNLSAL 172
QY 64 FDKTPEP 70
DB 173 FTKAPDP 179

RESULT 12
Q8ULY3 PRELIMINARY; PRT; 208 AA.
AC Q8ULY3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

```

```

RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126611; AAM95993.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 208
SQ SEQUENCE 208 AA; 23667 MW; 51211D59FAD690A6 CRC64;

Query Match 73.0%; Score 262; DB 12; Length 208;
Best Local Similarity 70.0%; Pred. No. 1.2e-22;
Matches 49; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFQHNLSAL 60
Db 110 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFQHNLSAL 169

QY 61 AAIFDKTPEP 70
Db 170 DRIFMKADKP 179

RESULT 13
Q8JLY5 PRELIMINARY; PRT; 289 AA.
AC Q8JLY5;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;
RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126610; AAM95993.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 289
SQ SEQUENCE 289 AA; 32971 MW; 4ECF52F4C69C6764 CRC64;

Query Match 73.0%; Score 262; DB 12; Length 289;
Best Local Similarity 70.0%; Pred. No. 1.8e-22;
Matches 49; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFQHNLSAL 60
Db 110 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFQHNLSAL 169

QY 61 AAIFDKTPEP 70
Db 170 DRIFMKADKP 179

RESULT 14
P88975 PRELIMINARY; PRT; 149 AA.
AC P88975;
DT 01-MAY-1997 (TremBLrel. 03, Created)
DT 01-MAY-1997 (TremBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;

```

```

RN SEQUENCE FROM N.A.
RP STRAIN=Jamaican;
RA Roye M.E.;
RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
DR EMBL; U75278; AAB36919.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 149
SQ SEQUENCE 149 AA; 16785 MW; E4CF5BED4C9CD508 CRC64;

Query Match 72.1%; Score 259; DB 12; Length 149;
Best Local Similarity 68.6%; Pred. No. 1.8e-22;
Matches 48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFQHNLSAL 60
Db 52 TIWGVFQIDGRSARGGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFQHNLSAL 111

QY 61 AAIFDKTPEP 70
Db 112 DRIFMKDPEP 121

RESULT 15
Q9YLA4 PRELIMINARY; PRT; 233 AA.
ID Q9YLA4;
AC Q9YLA4;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica strain 1;
RA Roye M.E.;
RT "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica strain 1;
RA Roye M.E., McLaughlin W.A., Maxwell D.P.;
RT "Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098940; RAD17850.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 233
SQ SEQUENCE 233 AA; 26356 MW; AA490AF4D2166A02 CRC64;

Query Match 72.1%; Score 259; DB 12; Length 233;
Best Local Similarity 68.6%; Pred. No. 3e-22;
Matches 48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFQHNLSAL 60
Db 110 TIWGVFQIDGRSARGGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFQHNLSAL 169

QY 61 AAIFDKTPEP 70
Db 170 DRIFMKDPEP 179

```

Search completed: December 23, 2003, 09:03:36
Job time : 25.3333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds
(without alignments)
340.128 Million cell updates/sec

Title: US-09-289-346B-8
Perfect score: 361
Sequence: 1 TLVNGEAAVDGRSARGGQCT.....PQFHNLNSLDRIFDKTPPEP 70

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq.19Jun03:*
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361	100.0	70	21 AAB18684	Mutant peptide der
2	350	97.0	70	21 AAB18677	Peptide fragment f
3	350	97.0	356	21 AAB18687	Amino acid sequenc
4	342	94.7	70	21 AAB18685	Mutant peptide der
5	339	93.9	70	21 AAB18688	Mutant peptide der
6	338	93.6	70	21 AAB18692	Mutant peptide der
7	336	93.1	70	21 AAB18690	Mutant peptide der
8	335	92.8	70	21 AAB18678	Mutant peptide der
9	335	92.8	70	21 AAB18686	Mutant peptide der

10	334	92.5	70	21 AAB18689	Mutant peptide der
11	332	92.0	70	21 AAB18680	Mutant peptide der
12	332	92.0	70	21 AAB18691	Mutant peptide der
13	329	91.1	70	21 AAB18681	Mutant peptide der
14	328	90.9	70	21 AAB18683	Mutant peptide der
15	326	90.3	70	21 AAB18682	Mutant peptide der
16	318	88.1	70	21 AAB18679	Mutant peptide der
17	223.5	61.9	50	23 AAO22043	Retinoblastoma-bin
18	216	59.8	353	18 AAW34338	Bean golden mosaic
19	216	59.8	353	18 AAW34332	Bean golden mosaic
20	216	59.8	353	18 AAW34333	Bean golden mosaic
21	216	59.8	353	18 AAW34334	Bean golden mosaic
22	216	59.8	353	18 AAW34335	Bean golden mosaic
23	216	59.8	359	17 AAR88870	Sardinian tomato y
24	216	59.8	359	17 AAR88871	Sardinian tomato y
25	216	59.8	359	17 AAR88872	Sardinian tomato y
26	214	59.3	353	8 AAP70407	ORF 4 gene product
27	214	59.3	361	18 AAW34336	Tomato mottle viru
28	214	59.3	361	18 AAW34324	Tomato mottle viru
29	214	59.3	361	18 AAW34325	Tomato mottle viru
30	214	59.3	361	18 AAW34326	Tomato mottle viru
31	212	58.7	357	18 AAW34329	Tomato yellow leaf
32	212	58.7	357	18 AAW34330	Tomato yellow leaf
33	212	58.7	357	18 AAW34331	Tomato yellow leaf
34	207.5	57.5	361	8 AAP70562	Product of ORF 4 f
35	204	56.5	357	18 AAW34337	Tomato yellow leaf
36	202	56.0	362	19 AAW56495	Tobacco leaf curl
37	101	28.0	142	24 ABP58120	Tomato yellow leaf
38	71.5	19.8	945	22 ABB65231	Drosophila melanog
39	68.5	19.0	1693	21 ABA48457	Human laminin 5 po
40	68.5	19.0	1693	21 ABA48459	Deduced sequence o
41	68.5	19.0	1713	21 AAR70148	Human laminin 5 po
42	68.5	19.0	1713	21 ABA48458	Human laminin 5 po
43	68.5	19.0	1724	21 ABA48456	Human laminin 5 po
44	66.5	18.4	512	19 AAW68473	HIV-1 strain YBF30
45	66.5	18.4	665	22 ABB70991	Drosophila melanog

ALIGNMENTS

RESULT 1

AAB18684
ID AAB18684 standard; peptide; 70 AA.

XX AAB18684;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 7 /note= "wild type residue replaced with Ala"

FT Misc-difference 8 /note= "wild type residue replaced with Ala"

XX WO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UUNC-) UNIV NORTH CAROLINA STATE.

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX DR WPI; 2000-618851/59.
 XX
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX
 XX Claim 52; Page 45; 73pp; English.
 XX
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 100.0%; Score 361; DB 21; Length 70;
 Best Local Similarity 100.0%; Pred. No. 8.7e-38;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLVWGEAAVDGRSARGCGCQTSNDAAALNASSKEEALQIIREKIPKYLQFQHNLSNL 60
 DB 1 TLVWGEAAVDGRSARGCGCQTSNDAAALNASSKEEALQIIREKIPKYLQFQHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 2
 AAB18677
 ID AAB18677 standard; peptide; 70 AA.
 AC AAB18677;
 XX
 XX 22-JAN-2001 (first entry)
 XX Peptide fragment from Rep protein of TGMV (amino acids 110-179).
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 XX Tomato golden mosaic virus.
 OS
 XX WO200054573-Al.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 XX
 XX 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX
 XX Disclosure; Page 18; 73pp; English.
 XX
 XX The present sequence is derived from a geminivirus replication (Rep)
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
 CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
 CC with other viral and host proteins. Mutants of the AL1 protein are used
 CC to produce transgenic plants. The mutation in AL1 is present in a
 CC ribosome binding region, and expression of mutant AL1 protein imparts
 CC increased resistance to geminivirus infection in the plant. Mutant AL1
 CC proteins are useful for producing plants having increased resistance or
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 CC beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 97.0%; Score 350; DB 21; Length 70;
 Best Local Similarity 97.1%; Pred. No. 2.1e-36;
 Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TLVWGEAAVDGRSARGCGCQTSNDAAALNASSKEEALQIIREKIPKYLQFQHNLSNL 60
 DB 1 TLVWGEAAVDGRSARGCGCQTSNDAAALNASSKEEALQIIREKIPKYLQFQHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 3
 AAB18687
 ID AAB18687 standard; peptide; 356 AA.
 AC AAB18687;
 XX
 XX 22-JAN-2001 (first entry)
 XX Amino acid sequence of a geminivirus replication protein of TGMV.
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 XX Tomato golden mosaic virus.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 354
 FT /note= "unspecified amino acid"
 XX
 XX WO200054573-Al.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 XX
 XX 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region


```

PT - encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
PS Disclosure; Page 48; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 93.9%; Score 339; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 5.2e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TLVWGEAAVDGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60
Db 1 TLVWGEFQVDRSARGGCAASNDAAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 6
AAB18692
ID AAB18692 standard; peptide; 70 AA.
AC AAB18692;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 66 /note= "wild type residue replaced with Ala"
FT FT
FT Misc-difference 69 /note= "wild type residue replaced with Ala"
FT FT
XX WO200054573-Al.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
PT

```

```

PT - encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
PS Disclosure; Page 50; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 93.6%; Score 338; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 6.9e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TLVWGEAAVDGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60
Db 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 7
AAB18690
ID AAB18690 standard; peptide; 70 AA.
AC AAB18690;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 27 /note= "wild type residue replaced with Ala"
FT FT
FT Misc-difference 30 /note= "wild type residue replaced with Ala"
FT FT
XX WO200054573-Al.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
PT

```

PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX
 XX
 XX Disclosure; Page 49; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA;
 SQ
 Query Match 93.1%; Score 336; DB 21; Length 70;
 Best Local Similarity 94.3%; Pred. No. 1.2e-34;
 Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TLVWGEAAVDGRSARGGCGTSDNDAAEALNASSKEALQIREKIPEKYLFOFHNLSNL 60
 DB 1 TLVWGEFQVDGRSARGGCGTSDNDAALAAASSKEALQIREKIPEKYLFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 8
 AAB18678
 ID AAB18678 standard; peptide; 70 AA.
 AC AAB18678;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 XX Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 XX FT Misc-difference 12 /note= "wild type residue replaced with Ala"
 XX FT Misc-difference 13 /note= "wild type residue replaced with Ala"
 XX FT Misc-difference 15 /note= "wild type residue replaced with Ala"
 XX FT Misc-difference 15 /note= "wild type residue replaced with Ala"
 XX
 XX WO200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 XX 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX

DR WPI; 2000-618851/59.
 XX
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 PT
 PT
 XX Claim 53; Page 42-43; 73pp; English.
 XX
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA;
 SQ
 Query Match 92.8%; Score 335; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 1.7e-34;
 Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TLVWGEAAVDGRSARGGCGTSDNDAAEALNASSKEALQIREKIPEKYLFOFHNLSNL 60
 DB 1 TLVWGEFQVDGAAAGGCGTSDNDAAEALNASSKEALQIREKIPEKYLFOFHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 9
 AAB18686
 ID AAB18686 standard; peptide; 70 AA.
 XX
 AC AAB18686;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 XX Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 XX FT Misc-difference 24 /note= "wild type residue replaced with Leu"
 XX FT Misc-difference 25 /note= "wild type residue replaced with Leu"
 XX FT Misc-difference 26 /note= "wild type residue replaced with Leu"
 XX FT Misc-difference 26 /note= "wild type residue replaced with Leu"
 XX
 XX WO200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 XX 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX

```

XX
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT
XX PS Claim 53; Page 46; 73pp; English.
XX
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX SQ Sequence 70 AA;
Query Match 92.8%; Score 335; DB 21; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.7e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 TLVWGEAAVDGRSARGCGQTSNDAAALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
Db 1 TLVWGEFQVDRSARGCGQTSNDLLLEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 10
AAB18689
ID AAB18689 standard; peptide; 70 AA.
AC AAB18689;
XX
XX DT 22-JAN-2001 (first entry)
XX
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 22 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX FT
XX FN WO200054573-A1.
XX
XX PD 21-SEP-2000.
XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX

```

```

PA
XX (UNNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT
XX PS Disclosure; Page 48-49; 73pp; English.
XX
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX SQ Sequence 70 AA;
Query Match 92.5%; Score 334; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 2.2e-34;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TLVWGEAAVDGRSARGCGQTSNDAAALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
Db 1 TLVWGEFQVDRSARGCGQTSAAAALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 11
AAB18680
ID AAB18680 standard; peptide; 70 AA.
AC AAB18680;
XX
XX DT 22-JAN-2001 (first entry)
XX
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 42 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 43 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 44 /note= "wild type residue replaced with Ala"
XX FT
XX FN WO200054573-A1.
XX
XX PD 21-SEP-2000.
XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX

```



```

PN WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX -
XX Claim 52; Page 44; 73pp; English.
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance to geminivirus infection in the
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX Sequence 70 AA;
XX Query Match 91.1%; Score 329; DB 21; Length 70;
XX Best Local Similarity 92.9%; Pred. No. 9.5e-34;
XX Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 TLVGEAAVDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 14
AAB18683
XX AAB18683 standard; peptide; 70 AA.
XX AC AAB18683;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX OS Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX FT Misc-difference 59 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 61 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 61 /note= "wild type residue replaced with Ala"

FT Misc-difference 62 /note= "wild type residue replaced with Ala"
XX WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX -
XX Claim 53; Page 45; 73pp; English.
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance to geminivirus infection in the
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX Sequence 70 AA;
XX Query Match 90.9%; Score 328; DB 21; Length 70;
XX Best Local Similarity 92.9%; Pred. No. 1.3e-33;
XX Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 TLVGEAAVDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 AAFDKTPEP 70
RESULT 15
AAB18682
XX AAB18682 standard; peptide; 70 AA.
XX AC AAB18682;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX OS Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX FT Misc-difference 52

```


Db 110 TIEWGQFQVDRSGRGQSQSANDSYAKALNADSIESTILTKBEQPKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70

Db 170 ERIFVKVPEP 179

RESULT 2

US-08-838-151A-46

; Sequence 46, Application US/08838151A

; Patent No. 6291743

; GENERAL INFORMATION:

; APPLICANT: Stout, John T

; APPLICANT: Luu, Hang T

; APPLICANT: Maxwell, Douglas

; APPLICANT: Ahlquist, Paul

; APPLICANT: Hanson, Steve

; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

; TITLE OF INVENTION: Genes

; NUMBER OF SEQUENCES: 63

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dressler, Rocky, Milnamow & Katz

; STREET: Two Prudential Plaza, Suite 4700

; CITY: Chicago

; STATE: Illinois

; COUNTRY: U.S.A.

; ZIP: 60601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/838,151A

; FILING DATE:

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Mueller, Lisa V

; REGISTRATION NUMBER: 38,978

; REFERENCE/DOCKET NUMBER: SVS3801P0260

; TELEPHONE: 312-616-5400

; TELEFAX: 312-616-5460

; INFORMATION FOR SEQ ID NO: 46:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 353 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-838-151A-46

Query Match 59.8%; Score 216; DB 3; Length 353;

Best Local Similarity 58.6%; Pred. No. 6.6e-20;

Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSGRGQSQSANDSYAKALNADSIESTILTKBEQPKDYVLQHHNIRSNL 60

Db 110 TIEWGQFQVDRSGRGQSQSANDSYAKALNADSIESTILTKBEQPKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70

Db 170 ERIFVKVPEP 179

RESULT 3

US-08-838-151A-49

; Sequence 49, Application US/08838151A

; Patent No. 6291743

; GENERAL INFORMATION:

; APPLICANT: Stout, John T

; APPLICANT: Luu, Hang T

; APPLICANT: Maxwell, Douglas

; APPLICANT: Ahlquist, Paul

; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

; TITLE OF INVENTION: Genes

; NUMBER OF SEQUENCES: 63

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dressler, Rocky, Milnamow & Katz

; STREET: Two Prudential Plaza, Suite 4700

; CITY: Chicago

; STATE: Illinois

; COUNTRY: U.S.A.

; ZIP: 60601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; APPLICANT: Hanson, Steve

; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

; TITLE OF INVENTION: Genes

; NUMBER OF SEQUENCES: 63

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dressler, Rocky, Milnamow & Katz

; STREET: Two Prudential Plaza, Suite 4700

; CITY: Chicago

; STATE: Illinois

; COUNTRY: U.S.A.

; ZIP: 60601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/838,151A

; FILING DATE:

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Mueller, Lisa V

; REGISTRATION NUMBER: 38,978

; REFERENCE/DOCKET NUMBER: SVS3801P0260

; TELEPHONE: 312-616-5400

; TELEFAX: 312-616-5460

; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 353 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-838-151A-49

Query Match 59.8%; Score 216; DB 3; Length 353;

Best Local Similarity 58.6%; Pred. No. 6.6e-20;

Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSGRGQSQSANDSYAKALNADSIESTILTKBEQPKDYVLQHHNIRSNL 60

Db 110 TIEWGQFQVDRSGRGQSQSANDSYAKALNADSIESTILTKBEQPKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70

Db 170 ERIFVKVPEP 179

RESULT 4

US-08-838-151A-52

; Sequence 52, Application US/08838151A

; Patent No. 6291743

; GENERAL INFORMATION:

; APPLICANT: Stout, John T

; APPLICANT: Luu, Hang T

; APPLICANT: Maxwell, Douglas

; APPLICANT: Ahlquist, Paul

; APPLICANT: Hanson, Steve

; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

; TITLE OF INVENTION: Genes

; NUMBER OF SEQUENCES: 63

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dressler, Rocky, Milnamow & Katz

; STREET: Two Prudential Plaza, Suite 4700

; CITY: Chicago

; STATE: Illinois

; COUNTRY: U.S.A.

; ZIP: 60601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-52

Query Match      59.8%; Score 216; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 6.6e-20;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVGEAAVDCRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 110 TIWGQFQVDCRSARGGCGQSANDSYAKALNADSIETALILKEQPKDYVLQHHNIRSL 169

QY 61 DRIFDKTPEP 70
   :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 ERIFFVKVPEP 179

RESULT 5
US-08-838-151A-55
; Sequence 55, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: protein
US-08-838-151A-55

Query Match      59.8%; Score 216; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 6.6e-20;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVGEAAVDCRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 110 TIWGQFQVDCRSARGGCGQSANDSYAKALNADSIETALILKEQPKDYVLQHHNIRSL 169

QY 61 DRIFDKTPEP 70
   :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 ERIFFVKVPEP 179

RESULT 6
US-08-809-103B-2
; Sequence 2, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-2

Query Match      59.8%; Score 216; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 6.7e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVNGEAAVDCRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 61
   :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 111 LEWGTQIDGRSARGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170

QY 62 RIFDKTPEP 70
   :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 171 KVFQVPPAP 179

RESULT 7

US-08-809-103B-4
; Sequence 4, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-4

Query Match 59.8%; Score 216; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 6.7e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEAAVDCRSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 61
Db 111 LEWGTFTQIDGRSARGGCGTNDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170
QY 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 8

US-08-809-103B-6
; Sequence 6, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-6

Query Match 59.8%; Score 216; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 6.7e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEAAVDCRSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 61
Db 111 LEWGTFTQIDGRSARGGCGTNDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170
QY 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 9

US-08-809-103B-8
; Sequence 8, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B

```
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8
;
; Query Match
; Best Local Similarity 59.8%; Score 216; DB 3; Length 359;
; Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
;
; QY 2 LVWGEAAVDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 61
; DB 111 LEWGTFTQIDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 170
;
; QY 62 RIFDKTPEP 70
; DB 171 KVFQVPPAP 179
;
; RESULT 10
; US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiiviruses
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
```

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-2
;
; Query Match
; Best Local Similarity 59.3%; Score 214; DB 3; Length 361;
; Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;
;
; QY 1 TLVWGEAAVDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 60
; DB 110 TIWGDFTQIDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 169
;
; QY 61 DRIFDKTPEP 70
; DB 170 ERIFAKAPEP 179
;
; RESULT 11
; US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiiviruses
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4
;
; Query Match
; Best Local Similarity 59.3%; Score 214; DB 3; Length 361;
; Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;
;
; QY 1 TLVWGEAAVDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 60
; DB 110 TIWGDFTQIDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 169
```



```

; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-24

Query Match      58.7%; Score 212; DB 3; Length 357;
Best Local Similarity 65.6%; Pred. No. 2.2e-19;
Matches 40; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY      4 WGEAAVDGSRAGGCGTSDNDAAAEALNASSKEEALQITREKIPKYLFPQFHNLSNLDRI 63
Db      111 FGVSIQDGRSARGGQGSANDAYAEALNSGSKSEALNILEKAPKDYILOFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

Search completed: December 23, 2003, 08:59:35
Job time : 11.6667 secs

; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-27

Query Match      58.7%; Score 212; DB 3; Length 357;
Best Local Similarity 65.6%; Pred. No. 2.2e-19;
Matches 40; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY      4 WGEAAVDGSRAGGCGTSDNDAAAEALNASSKEEALQITREKIPKYLFPQFHNLSNLDRI 63
Db      111 FGVSIQDGRSARGGQGSANDAYAEALNSGSKSEALNILEKAPKDYILOFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

RESULT 15
US-08-838-151A-27
; Sequence 27, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-27
```

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds
(without alignments)
172.015 Million cell updates/sec

Title: US-09-289-346B-8
Perfect score: 361
Sequence: 1 TLVWGEAAVDSARGGCQT.....POFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues
Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361	100.0	70	10	US-09-289-346A-8
2	350	97.0	70	10	US-09-289-346A-1
3	350	97.0	356	10	US-09-289-346A-11
4	342	94.7	70	10	US-09-289-346A-9
5	339	93.9	70	10	US-09-289-346A-12
6	338	93.6	70	10	US-09-289-346A-16
7	336	93.1	70	10	US-09-289-346A-14
8	335	92.8	70	10	US-09-289-346A-2
9	335	92.8	70	10	US-09-289-346A-10
10	334	92.5	70	10	US-09-289-346A-13
11	332	92.0	70	10	US-09-289-346A-4
12	332	92.0	70	10	US-09-289-346A-15
13	329	91.1	70	10	US-09-289-346A-5
14	328	90.9	70	10	US-09-289-346A-7
15	326	90.3	70	10	US-09-289-346A-6

16	318	88.1	70	10	US-09-289-346A-3
17	68.5	19.0	1713	15	US-10-171-311-113
18	66.5	18.4	512	12	US-10-301-661A-4
19	65	18.0	293	15	US-10-151-336-3
20	65	18.0	335	15	US-10-151-336-6
21	63.5	17.6	447	9	US-09-989-722-369
22	63.5	17.6	447	9	US-09-989-723-369
23	63.5	17.6	447	9	US-09-989-279-369
24	63.5	17.6	447	9	US-09-989-727-369
25	63.5	17.6	447	10	US-09-989-731-369
26	63.5	17.6	447	10	US-09-989-732-369
27	63.5	17.6	447	10	US-09-991-073-369
28	63.5	17.6	447	10	US-09-990-442-369
29	63.5	17.6	447	10	US-09-991-163-369
30	63.5	17.6	447	10	US-09-993-604-369
31	63.5	17.6	447	10	US-09-990-456-369
32	63.5	17.6	447	10	US-09-989-721-369
33	63.5	17.6	447	10	US-09-992-598-369
34	63.5	17.6	447	10	US-09-989-293A-369
35	63.5	17.6	447	10	US-09-989-735-369
36	63.5	17.6	447	10	US-09-990-444-369
37	63.5	17.6	447	10	US-09-991-181-369
38	63.5	17.6	447	10	US-09-989-730-369
39	63.5	17.6	447	10	US-09-990-436-369
40	63.5	17.6	447	10	US-09-993-687-369
41	63.5	17.6	447	11	US-09-989-734-369
42	63.5	17.6	447	11	US-09-997-653-369
43	63.5	17.6	447	11	US-09-993-667-369
44	63.5	17.6	447	11	US-09-997-428-369
45	63.5	17.6	447	11	US-09-997-666-369

ALIGNMENTS

RESULT 1
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT FILING DATE: 1999-04-09
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AAl18).

Query Match	100.0%	Score 361;	DB 10;	Length 70;
Best Local Similarity	100.0%	Pred. No. 3.3e-36;		
Matches	70;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
QY	1	TLVWGEAAVDSARGGCQTSDNAAALNASSKEALQIIREKIPKYLQFHHNLSNL	60	
Db	1	TLVWGEAAVDSARGGCQTSDNAAALNASSKEALQIIREKIPKYLQFHHNLSNL	60	
QY		61 DRIFDKTPEP	70	

```
Db      61 DRIFDKTPEP 70
|||||
110 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 169

RESULT 2
US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRF
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1

Query Match      97.0%; Score 350; DB 10; Length 70;
Best Local Similarity 97.1%; Pred. No. 8.2e-37;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TLVWGEAAVDGRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db      1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Qy      61 DRIFDKTPEP 70
|||||
61 DRIFDKTPEP 70

RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRF
; ORGANISM: Tomato golden mosaic virus
; FEATURE: UNSURE
; NAME/KEY: (354)
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match      97.0%; Score 350; DB 10; Length 356;
Best Local Similarity 97.1%; Pred. No. 6.8e-36;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TLVWGEAAVDGRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
|||||

Query Match      93.9%; Score 339; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 8.5e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 TLVWGEAAVDGRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db      1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Qy      61 DRIFDKTPEP 70
|||||
61 DRIFDKTPEP 70

RESULT 4
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRF
; ORGANISM: Tomato golden mosaic virus
; FEATURE: VARIANT
; NAME/KEY: (10)
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match      94.7%; Score 342; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 8.5e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 TLVWGEAAVDGRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db      1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Qy      61 DRIFDKTPEP 70
|||||
61 DRIFDKTPEP 70

RESULT 5
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRF
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12
```


Query Match 93.1%; Score 336; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 4.9e-35;

```

RESULT 9
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT

```

```
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)...(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAAI36->LLLI36).
US-09-289-346A-10

Query Match          92.8%; Score 335; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 6.5e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGEAAVDGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVDCRSARGGCGQTSNDLLLEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-13

Query Match          92.5%; Score 334; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 8.8e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TLVWGEAAVDGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVDCRSARGGCGQTSAAAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
```

```
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (42)...(44)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REKI54->AAAI54).
US-09-289-346A-4

Query Match          92.0%; Score 332; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.6e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGEAAVDGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVDCRSARGGCGQTSNDAAAEALNASSKEEALQIIRAAIPEKYLQFHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match          92.0%; Score 332; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.6e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGEAAVDGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVDCRSARGGCGQTSNDAAAEALNASSAAAAALQIIREKIPEKYLQFHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
```

```
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 60/125,004
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (SKY159->AAA159).
US-09-289-346A-5

Query Match          91.1%; Score 329; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 3.8e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TLVWGEFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 DRIFDKTPEP 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 DRIFDKTPEP 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDRI72->ALAA172).
US-09-289-346A-7

Query Match          90.9%; Score 328; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 5e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TLVWGEFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSAL 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 DRIFDKTPEP 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AAIIDKTPEP 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 15
US-09-289-346A-6
; Sequence 6, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (52)..(55)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (QFHN165->AFPA165).
US-09-289-346A-6
```

```
Query Match          90.3%; Score 326; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 9e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TLVWGEFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 DRIFDKTPEP 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 DRIFDKTPEP 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: December 23, 2003, 09:43:31
Job time : 77 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.7778 Seconds
(without alignments)
569.747 Million cell updates/sec

Title: US-09-289-346B-8

Perfect score: 361

Sequence: 1 TLVNGEAAVDGRSARGGCGT.....PQHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	350	97.0	352	1 VAL1_TGMV	P03567 tomato gold
2	250	69.3	361	1 VAL1_PYMV	P27258 potato yell
3	237	65.7	358	1 VAL1_CIVK	P14982 cassava lat
4	237	65.7	358	1 VAL1_CIVN	P14972 cassava lat
5	230	63.7	362	1 VAL1_TYLC	P36279 tomato yell
6	223	61.8	359	1 VAL1_TYLC	P38609 tomato yell
7	219	60.7	349	1 VAL1_PHVU	P06923 pepper huas
8	216	59.8	359	1 VAL1_TYLC	P27260 tomato yell
9	214	59.3	353	1 VAL1_BGMV	P05175 bean golden
10	213	59.0	355	1 VAL1_ABMV	P21947 abutilon mo
11	212	58.7	357	1 VAL1_TYLC	P27259 tomato yell
12	210	58.2	358	1 VAL1_BCTV	P14991 beet curly
13	210	58.2	361	1 VAL1_TMGV	P06657 tomato mott
14	117	32.4	347	1 VAL1_SUCV	P29048 squash leaf
15	68.5	19.0	1713	1 LMA3_HUMAN	Q16787 homo sapien
16	65.5	18.1	298	1 OLG2_CHICK	Q90xb3 gallus gall
17	64.5	17.9	299	1 Y175_HELPJ	Q9zmq7 helicobacte
18	63.5	17.6	447	1 TBL2_HUMAN	Q9v4p3 homo sapien
19	63.5	17.6	1610	1 CCAD_MESAU	Q99244 mesocricetu
20	63.5	17.6	2161	1 CCAD_HUMAN	Q01868 homo sapien
21	63.5	17.6	2203	1 CCAD_RAT	P27732 rattus norv
22	62	17.2	295	1 VAL1_TYDV	P31617 tobacco yell
23	61	16.9	1502	1 CYP1_YEAST	P12351 saccharomyc
24	60	16.6	432	1 PROA_DEIRA	Q9rtcd9 deinococcus
25	60	16.6	447	1 CDSA_DROME	P56079 d phosphati
26	59.5	16.5	136	1 Y452_CABEL	O62250 caenorhabdi
27	59.5	16.5	299	1 Y175_HELPJ	P56112 helicobacte
28	59.5	16.5	476	1 DGRE_HUMAN	Q96df8 homo sapien
29	59.5	16.5	479	1 DGRE_MOUSE	O70279 mus musculu
30	59	16.3	640	1 DNAX_RHOMR	Q9xcbl1 rhodothermu
31	59	16.3	747	1 YU20_MOUSE	Q9wv70 mus musculu
32	58.5	16.2	297	1 RRPV_RABVP	P06747 rabies viru
33	58.5	16.2	334	1 G3P_EACST	P00362 bacillus st

RESULT 1
VAL1_TGMV STANDARD; PRT; 352 AA.
AC P03567;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Tomato golden mosaic virus (TGMV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10831;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;
RT "Complete nucleotide sequence of the infectious cloned DNA components
of tomato golden mosaic virus: potential coding regions and regulatory
sequences.";
RL EMBL J. 3:2197-2205(1984).
CC - SIMILARITY: BELONGS TO GEMINIVIRUS ALL PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
EMBL; K02029; -; NOT_ANNOTATED_CDS.
DR PIR; A04170; QOCVLI.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATAL1.
DR PRODOM; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 223 230 ATP (POTENTIAL).
SQ SEQUENCE 352 AA; 40332 MW; C33C938E9644B4A4 CRC64;
Query Match 97.0%; Score 350; DB 1; Length 352;
Best Local Similarity 97.1%; Pred. No. 5.7e-32;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TLVNGEAAVDGRSARGGCGTSDNAAAEALNASSKEALQIIREKIPKYLQFPHNLNSL 60
Db 111 TLVNGEFOVDGRSARGGCGTSDNAAAEALNASSKEALQIIREKIPKYLQFPHNLNSL 170
QY 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180
RESULT 2
VAL1_PYMV
ID VAL1_PYMV STANDARD; PRT; 361 AA.
AC P27258;

P15115 bacillus co
P28868 candida alb
Q82064 anabaena sp
P45221 haemophilus
O94751 echizoaecch
P42338 homo sapien
Q99r35 staphylococ
Q8num9 staphylococ
P36682 escherichia
P49052 bacillus li
Q8dfj1 vibrio vuln
Q9cfig7 lactococcus

ALIGNMENTS

```
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D00940; BAA00782.1; -.
DR PIR; J00364; Q0CVPT.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW NP_BIND. 222 229 ATP (POTENTIAL).
FT SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;
SQ
Query Match 69.3%; Score 250; DB 1; Length 361;
Best Local Similarity 68.1%; Pred. No. 1e-20;
Matches 47; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGQTSDAAAEALNASKEALQIIREKIPKYLQFHNLSNL 60
Db 110 TIEWGLFQIDGRSARGCGQTSDAAAEALNASKEALQIIREKIPKYLQFHNLSNL 169
QY 61 DRIFDKTPE 69
Db 170 DRIFDKAPE 178

RESULT 3
VAL1 CLVK
ID VAL1 CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA."
RL Nature 301:260-262(1983).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
```

```
CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND. 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753EB92D69 CRC64;

Query Match 65.7%; Score 237; DB 1; Length 358;
Best Local Similarity 61.4%; Pred. No. 3e-19;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGQTSDAAAEALNASKEALQIIREKIPKYLQFHNLSNL 60
Db 109 TVEWGQFQIDGRSARGCGQTSDAAAEALNASKEALQIIREKIPKYLQFHNLSNL 168
QY 61 DRIFDKTPE 70
Db 169 DRIFQBPAP 178

RESULT 4
VAL1 CLVN
ID VAL1 CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain)."
RL Nucleic Acids Res. 18:197-198(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X17095; CAA34953.1; -.
DR PIR; S07594; S07594.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND. 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16BB0CB2D5E2C CRC64;

Query Match 65.7%; Score 237; DB 1; Length 358;
Best Local Similarity 61.4%; Pred. No. 3e-19;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGQTSDAAAEALNASKEALQIIREKIPKYLQFHNLSNL 60
Db 109 TVEWGQFQIDGRSARGCGQTSDAAAEALNASKEALQIIREKIPKYLQFHNLSNL 168
QY 61 DRIFDKTPE 70
Db 169 DRIFQBPAP 178
```

```

RESULT 5
VAL1 TYLCA
ID VAL1 TYLCA STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxID=36447;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Rigden J.E., Krake L.R., Mullineux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
  geminivirus.";
RL J. Gen. Virol. 74:147-151(1993).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR PIR; JQ1887; JQ1887.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 63.7%; Score 230; DB 1; Length 362;
Best Local Similarity 54.1%; Pred. No. 1.8e-18;
Matches 46; Conservative 9; Mismatches 14; Indels 16; Gaps 1;

QY 1 TLVGEAAVDGRSARGGCGQTSDNDAAEALNASSKEALQIIRKIKEKYLQFHNLSNLD 60
DB 110 TLWGEFQIDGRSARGGCGQTANDAYAKAINAGSKSEALDVIKELAPRDYILHFNHNSNLD 170

QY 61 DRI-----FDKTPPE 69
DB 170 DRIPTPEVVVSPFLSSSFDVRPE 194

RESULT 6
VAL1 TYLCA
ID VAL1 TYLCA STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Norris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
  from the west Mediterranean basin: the nucleotide sequence of an
  infectious clone from Spain.";
RL Arch. Virol. 135:165-170(1994).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR PIR; JQ2300; JQ2300.
DR PIR; S31875; S31875.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 39722 MW; D5F4E76CD56370F4 CRC64;

Query Match 60.7%; Score 219; DB 1; Length 349;
Best Local Similarity 58.6%; Pred. No. 3e-17;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVGEAAVDGRSARGGCGQTSDNDAAEALNASSKEALQIIRKIKEKYLQFHNLSNLD 60
DB 110 TLWGEFQIDGRSARGGCGQTANDAYAKAINAGSKSEALDVIKELAPRDYILHFNHNSNLD 169

CC
EMBL; Z25751; CAA81026.1; -.
DR PIR; S39211; S39211.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A38C CRC64;

Query Match 61.8%; Score 223; DB 1; Length 359;
Best Local Similarity 59.4%; Pred. No. 1.1e-17;
Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEAAVDGRSARGGCGQTSDNDAAEALNASSKEALQIIRKIKEKYLQFHNLSNLD 61
DB 111 LEWTFQIDGRSARGGCGQTANDAYAKAINAGSKSEALDVIKELAPRDYILHFNHNSNLD 170

QY 62 RIFDKTPPE 70
DB 171 RVFQVPPAP 179

RESULT 7
VAL1 PHUV
ID VAL1 PHUV STANDARD; PRT; 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AL1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Betrella L.,
  Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
  comparison with bipartite geminiviruses.";
RL J. Gen. Virol. 74:2225-2231(1993).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC EMBL; X70418; CAA49856.1; -.
DR PIR; JQ2300; JQ2300.
DR PIR; S31875; S31875.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 39722 MW; D5F4E76CD56370F4 CRC64;

Query Match 60.7%; Score 219; DB 1; Length 349;
Best Local Similarity 58.6%; Pred. No. 3e-17;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVGEAAVDGRSARGGCGQTSDNDAAEALNASSKEALQIIRKIKEKYLQFHNLSNLD 60
DB 110 TLWGEFQIDGRSARGGCGQTANDAYAKAINAGSKSEALDVIKELAPRDYILHFNHNSNLD 169

```

```

QY 61 DRIFDKTPEP 70
Db 170 NRIFQTPPEP 179

RESULT 8
VAL1_TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92107660; PubMed=1840676;
RA Khey-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a
RT whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; M10070; AAA46318.1; -
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 59.8%; Score 216; DB 1; Length 359;
Best Local Similarity 56.5%; Pred. No. 6.8e-17;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEAAVDGRSGCGQTSNDAAAEALNASSKEEALQIREKIPEKYLFOFHNLSNLD 61
Db 111 LEWGTFOIGRSARGGQQTANDAYAKAINAGSKQALDVIKELAPRDYVLHFHNLSNLD 170
QY 62 RIPEKTPPEP 70
Db 171 KVQVPPPEP 179

RESULT 9
VAL1_BGMV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE AL1 protein (40.2 kDa protein).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimmatt G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; X15983; -; NOT_ANNOTATED_CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.

SEQUENCE FROM N.A.
RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
RT regulation in geminiviruses";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; M10070; AAA46318.1; -
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 59.3%; Score 214; DB 1; Length 353;
Best Local Similarity 58.6%; Pred. No. 1.1e-16;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSGCGQTSNDAAAEALNASSKEEALQIREKIPEKYLFOFHNLSNLD 60
Db 110 TIEWGQPVQDGRSGGQGSANDSYAKALNADSIESALTILKEBQPKDYVLQNHNRSLN 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFFKVPEP 179

RESULT 10
VAL1_ABMVW STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimmatt G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; X15983; -; NOT_ANNOTATED_CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.

```

```

FT NP BIND      221      228      ATP (POTENTIAL).
SQ SEQUENCE     355 AA; 40257 MW; 16A2CA8A63251E95 CRC64;

Query Match
Best Local Similarity 59.0%; Score 213; DB 1; Length 355;
Matches 40; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 1 TLVWGAADVGRSARGGQTSNDAAALNASSKEALQIREKIPKYLFOFHNLSNL 60
Db 110 TLWGEFQIDGRSARGGQTSNDAAALNASSKEALQIREKIPKYLFOFHNLSNL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 11
VAL1_TYLCV
ID VAL1_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9204070; PubMed=1926771;
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RL with a single genomic component.";
RL Virology 185:151-161(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X15656; CA933688.1; -.
CC PIR; D40779; QQCVC1.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
CC NP BIND      219      226      ATP (POTENTIAL).
SQ SEQUENCE     357 AA; 40678 MW; 939AB68E1AE3B2A7 CRC64;

Query Match
Best Local Similarity 58.7%; Score 212; DB 1; Length 357;
Matches 40; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 4 WGAADVGRSARGGQTSNDAAALNASSKEALQIREKIPKYLFOFHNLSNLDRI 63
Db 111 FGVSQIDGRSARGGQTSNDAAALNASSKEALQIREKIPKYLFOFHNLSNLDRI 170
QY 64 F 64
Db 171 F 171

RESULT 12
VAL1_BCTV
ID VAL1_BCTV STANDARD; PRT; 358 AA.
AC P14991;
DT 01-APR-1990 (Rel. 14, Created)

```

```

DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
RT beet curly top virus".
RL EMBL J. 5:1761-1767(1986).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X04144; -. NOT ANNOTATED CDS.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
CC NP BIND      222      229      ATP (POTENTIAL).
SQ SEQUENCE     358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match
Best Local Similarity 58.2%; Score 210; DB 1; Length 358;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGAADVGRSARGGQTSNDAAALNASSKEALQIREKIPKYLFOFHNLSNL 60
Db 110 TLWGEFQIDGRSARGGQTSNDAAALNASSKEALQIREKIPKYLFOFHNLSNL 169
QY 61 DRIFDKTPEP 70
Db 170 QKIFQRPDP 179

RESULT 13
VAL1_TMOV
ID VAL1_TMOV STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AL1.
OS Tomato mottle virus (isolate Florida) (TMov).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93107858; PubMed=1469361;
RA Abouzid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida.";
RL J. Gen. Virol. 73:3225-3229(1992).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC

```



```

DR EMBL; L14460; AAC32414.1; -.
DR PIR; JQ1870.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 8138B65CEEAC6950 CRC64;

Query Match 58.2%; Score 210; DB 1; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.3e-16;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVGEADVGRSARGGCGTSDNAAAEALNASSKEEALQIREKIPKYLQFHNLSNL 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 110 TIEWDFQIDGRSARGGCGTSDNAAAEALNASSKEEALQIREKIPKYLQFHNLSNL 169

Qy 61 DRIPDKTPEP 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 ERIFAKAPEP 179

RESULT 14
ID VAL1_SLCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RA Lazarowitz S.G.; Lazdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype.";
RL Virology 180:58-69(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M38183; AAC32410.1; ALT_INIT.
DR PIR; C36785; QOCVSI.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDABDDDE122110E CRC64;

Query Match 32.4%; Score 117; DB 1; Length 347;
Best Local Similarity 37.9%; Pred. No. 9e-06;
Matches 25; Conservative 12; Mismatches 25; Indels 4; Gaps 1;

Qy 5 GEADVGRSARGGCGTSDNAAAEALNASSKEEALQIREKIPKYLQFHNLSNLDRI 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 116 GQKVGSG----GSKSNKDDVYHNAVAGSAGEALDIKAGDKPTFIYVYHLLANVELP 171

Qy 65 DKTPPEP 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 QKPEP 177

```

RESULT 15

```

ID LMA3_HUMAN STANDARD; PRT; 1713 AA.
AC Q16787; Q13679; Q13680;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Laminin alpha-3 chain precursor (Epiligrin 170 kDa subunit) (E170)
DE (Nicein alpha subunit).
GN LMA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=keratinocytes;
RX MEDLINE=94357926; PubMed=8077230;
RA Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
RT "Cloning of the Lama3 gene encoding the alpha 3 chain of the adhesive
RT ligand epiligrin. Expression in wound repair.";
RL J Biol. Chem. 269:22779-22787(1994).
RN [2]
RP SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=96163880; PubMed=8586427;
RA Vidal F., Baudoin C., Miquel C., Galliano M.-F., Christiano A.M.,
RA Utito J., Ortonne J.-P., Meneguzzi G.;
RT "Cloning of the laminin alpha 3 chain gene (LAMA3) and identification
RT of a homozygous deletion in a patient with Herlitz junctional
RT epidermolysis bullosa.";
RL Genomics 30:273-280(1995).
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -1- FUNCTION: LAMININ-5 IS THOUGHT TO BE INVOLVED IN (1) CELL ADHESION
CC VIA INTEGRIN ALPHA-3/BETA-1 IN FOCAL ADHESION AND INTEGRIN ALPHA-
CC 6/BETA-4 IN HEMIDESMOSOMES, (2) SIGNAL TRANSDUCTION VIA TYROSINE
CC PHOSPHORYLATION OF PPI25-FAK AND P80, (3) DIFFERENTIATION OF
CC KERATINOCYTES.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The alpha-3 chain is a subunit of laminin-5
CC (epiligrin/kalinin/nicein), and possibly also a component of
CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC MEMBRANES (MAJOR COMPONENT).
CC -1- ALTERNATIVE PRODUCTS:
CC Name=A;
CC IsoId=Q16787-1; Sequence=Displayed;
CC Name=B;
CC IsoId=Q16787-2; Sequence=VSP_003037;
CC Note=Sequence incomplete;
CC -1- TISSUE SPECIFICITY: SKIN; RESPIRATORY, URINARY, AND DIGESTIVE
CC EPITHELIA AND IN OTHER SPECIALIZED TISSUES WITH PROMINENT
CC SECRETORY OR PROTECTIVE FUNCTIONS. EPITHELIAL BASEMENT MEMBRANE,
CC AND EPITHELIAL CELL TONGUE THAT MIGRATES INTO A WOUND BED. A
CC DIFFERENTIAL AND FOCAL EXPRESSION OF THE ALPHA-3 CHAIN IS OBSERVED
CC IN THE CNS.
CC -1- INDUCTION: LAMININ-5 IS UP-REGULATED IN WOUND SITES OF HUMAN SKIN.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAIN G IS GLOBULAR.
CC -1- DISEASE: DEFECTS IN LAMA3 ARE A CAUSE OF JUNCTIONAL EPIDERMOLYSIS
CC BULLOSA (JEB) GRAVIS, ALSO KNOWN AS HERLITZ TYPE JEB. IT IS A
CC BLISTERING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION
CC OF BASAL CELLS FROM THE BASEMENT MEMBRANE DUE TO A DECREASED
CC NUMBER OF HEMIDESMOSOMES. LAMININ-5 IS MISSING FROM THE BASEMENT

```


1

Result No.	Score	Query #		Length	DB	ID	Description
		Match					
1	301	83.4		351	12	Q91R10	Q91r10 tomato seve
2	299	82.8		352	12	Q9E000	Q9E000 tomato rugo
3	291	80.6		322	12	Q8QPv3	Q8qpV3 tomato chlo
4	282	78.1		226	12	Q9WHF6	Q9whf6 tomato mild
5	282	78.1		226	12	Q09727	Q09727 leonurus mo
6	280	77.6		361	12	Q67574	Q67574 bean golden
7	278	77.0		225	12	Q9QD81	Q9qdb1 cowpea gold
8	278	77.0		314	12	Q9ELT8	Q9elt8 sweet potat
9	278	77.0		264	12	Q3Q555	Q3q555 sweet potat
10	275	76.2		185	12	Q98693	Q98693 sida golden
11	271	75.1		235	12	Q8QPu4	Q8qpU4 tomato infe
12	270	74.8		208	12	Q8JLY3	Q8jly3 potato yell
13	270	74.8		289	12	Q8JLY5	Q8jly5 potato yell
14	267	74.0		149	12	P88975	P88975 macroptiliu
15	267	74.0		233	12	Q9YLA4	Q9yla4 macroptiliu
16	266	73.7		361	12	Q8JmI4	Q8jmi4 potato yell

1

Result No.	Score	Query #		Length	DB	ID	Description
		Match					
1	301	83.4		351	12	Q91R10	Q91r10 tomato seve
2	299	82.8		352	12	Q9E000	Q9E000 tomato rugo
3	291	80.6		322	12	Q8QPv3	Q8qpV3 tomato chlo
4	282	78.1		226	12	Q9WHF6	Q9whf6 tomato mild
5	282	78.1		226	12	Q09727	Q09727 leonurus mo
6	280	77.6		361	12	Q67574	Q67574 bean golden
7	278	77.0		225	12	Q9QD81	Q9qdb1 cowpea gold
8	278	77.0		314	12	Q9ELT8	Q9elt8 sweet potat
9	278	77.0		264	12	Q3Q555	Q3q555 sweet potat
10	275	76.2		185	12	Q98693	Q98693 sida golden
11	271	75.1		235	12	Q8QPu4	Q8qpU4 tomato infe
12	270	74.8		208	12	Q8JLY3	Q8jly3 potato yell
13	270	74.8		289	12	Q8JLY5	Q8jly5 potato yell
14	267	74.0		149	12	P88975	P88975 macroptiliu
15	267	74.0		233	12	Q9YLA4	Q9yla4 macroptiliu
16	266	73.7		361	12	Q8JmI4	Q8jmi4 potato yell


```

SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;
Query Match 78.1%; Score 282; DB 12; Length 226;
Best Local Similarity 78.6%; Pred. No. 3e-24;
Matches 55; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGCQTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 111 TWVGEFQVDRSGSRGCGQTVDAAAEALNAPDKRTALQIIEKLPKYLFOFHNLSNL 170

QY 61 DRIFDKTPEP 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 171 DRIFAKAPEP 180

RESULT 6
ID Q67574 PRELIMINARY; PRT; 361 AA.
AC Q67574;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative replicative protein.
GN Ali.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
   Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
   geminiviruses and determining their infectivity by electric discharge
   particle acceleration.";
RL Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
   Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
   hybridization probes and aspects of bean golden mosaic in Brazil.";
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
   disease: The nucleotide sequence of the infectious cloned DNA
   components of a Brazilian isolate of bean golden mosaic geminivirus.";
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M88686; AAA46312.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 77.6%; Score 280; DB 12; Length 361;
Best Local Similarity 77.6%; Pred. No. 8.9e-24;
Matches 52; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 4 WGEAAVDGRSARGCGCQTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 WGFQVDRSGSRGCGQTANDAAAEALNASSKEEAMQIIEKLPKYLFOFHNLSNLDRI 172

QY 64 FDKTPEP 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 FTKAPDP 179

RESULT 7
Q9QDB1 PRELIMINARY; PRT; 225 AA.
ID Q9QDB1
AC Q9QDB1;

```

```

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Replication associated protein (Fragment).
GN REF.
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CGMV-BR;
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
   Brazil.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF188708; AAF06318.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 225 225
SQ SEQUENCE 225 AA; 25766 MW; 1089CB6BD8D15BSD CRC64;

Query Match 77.0%; Score 278; DB 12; Length 225;
Best Local Similarity 77.6%; Pred. No. 8.5e-24;
Matches 52; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 WGEAAVDGRSARGCGCQTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 WGFQVDRSGSRGCGQTINDAAAEALNASSKEEAMQIIEKLPKYLFOFHNLSNLDRI 172

QY 64 FDKTPEP 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 FKKPPEP 179

RESULT 8
Q9ELT8 PRELIMINARY; PRT; 314 AA.
ID Q9ELT8
AC Q9ELT8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Replication association protein.
GN ACL.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
   States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288227; AAG01006.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 77.0%; Score 278; DB 12; Length 314;
Best Local Similarity 80.9%; Pred. No. 1.3e-23;
Matches 55; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGCQTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 110 TITWGEFQVDRSGSRGCGQTANDAAAEALNASSKEEALQIIREKLPKYLFOFHNLSNL 169

```

```

QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 9
Q9Q55 PRELIMINARY; PRT; 364 AA.
AC Q9Q55;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RT virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0 (1999).
DR EMBL; AF104036; AAD47173.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 77.0%; Score 278; DB 12; Length 364;
Best Local Similarity 80.9%; Pred. No. 1.5e-23;
Matches 55; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGSRAGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
Db 110 TIWGEFQDGRSARGGQQTANDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 169

QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Rep protein (fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-Jamaica;
RA Roye M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed
RT species Sida spp, Macroptilium lathyroides, and Wissadula amplissima
RT from Jamaica.";
RL Plant Dis. 81:1251-1258 (1997).
DR EMBL; U67926; AAB97865.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.

QY ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 185 AA; 20975 MW; 3913850A025A5EE1 CRC64;

Query Match 76.2%; Score 275; DB 12; Length 185;
Best Local Similarity 71.4%; Pred. No. 1.5e-23;
Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGSRAGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
Db 89 TIWGEFQDGRSARGGQQTANDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 148

QY 61 DRIFDKTP 70
Db 149 DRIFSKPP 158

RESULT 11
Q8QPU4 PRELIMINARY; PRT; 235 AA.
AC Q8QPU4;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Replication-associated protein (fragment).
GN AC1.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=MG-B11;
RA Ribeiro S.G., Ambrozovicus L.P., de Avila A.C., Calegario R.F.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049208; AAL82833.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR ProDom; PD000736; Gemini_AL1; 1.
DR Non TER 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BE0DD9C810 CRC64;

Query Match 75.1%; Score 271; DB 12; Length 235;
Best Local Similarity 74.6%; Pred. No. 5.7e-23;
Matches 50; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 4 WGEAAVDGSRAGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 63
Db 113 WGIFQIDGRSARGGQQTANDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 172

QY 64 DRIFDKTP 70
Db 173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Replication-associated protein (fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

```

1

Search completed: December 23, 2003, 09:03:37
Job time : 26.3333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds
(without alignments)
340.128 Million cell updates/sec

Title: US-09-289-346B-9

Perfect score: 362

Sequence: 1 TLVMEFQVAGSARGGCT.....FQHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1_ /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	362	100.0	70	21 AAB18685	Mutant peptide der
2	356	98.3	70	21 AAB18677	Peptide fragment f
3	356	98.3	356	21 AAB18687	Amino acid sequenc
4	345	95.3	70	21 AAB18688	Mutant peptide der
5	344	95.0	70	21 AAB18692	Mutant peptide der
6	342	94.5	70	21 AAB18684	Mutant peptide der
7	342	94.5	70	21 AAB18690	Mutant peptide der
8	341	94.2	70	21 AAB18678	Mutant peptide der
9	341	94.2	70	21 AAB18686	Mutant peptide der

10	340	93.9	70	21 AAB18689	Mutant peptide der
11	338	93.4	70	21 AAB18680	Mutant peptide der
12	338	93.4	70	21 AAB18691	Mutant peptide der
13	335	92.5	70	21 AAB18681	Mutant peptide der
14	334	92.3	70	21 AAB18683	Mutant peptide der
15	332	91.7	70	21 AAB18682	Mutant peptide der
16	324	89.5	70	21 AAB18679	Mutant peptide der
17	223.5	61.7	50	23 AAO22043	Retinoblastoma-bin
18	222	61.3	353	18 AAW34338	Bean golden mosaic
19	222	61.3	353	18 AAW34332	Bean golden mosaic
20	222	61.3	353	18 AAW34333	Bean golden mosaic
21	222	61.3	353	18 AAW34334	Bean golden mosaic
22	222	61.3	353	18 AAW34335	Bean golden mosaic
23	222	61.3	359	17 AAR88870	Sardinian tomato y
24	222	61.3	359	17 AAR88871	Sardinian tomato y
25	222	61.3	359	17 AAR88872	Sardinian tomato y
26	220	60.8	353	8 AAP70407	ORF 4 gene product
27	220	60.8	361	18 AAW34336	Tomato mottle viru
28	220	60.8	361	18 AAW34324	Tomato mottle viru
29	220	60.8	361	18 AAW34325	Tomato mottle viru
30	220	60.8	361	18 AAW34326	Tomato mottle viru
31	213.5	59.0	361	8 AAP70562	Product of ORF 4 f
32	208	57.5	362	19 AAW56495	Tobacco leaf curl
33	207	57.2	357	18 AAW34329	Tomato yellow leaf
34	207	57.2	357	18 AAW34330	Tomato yellow leaf
35	207	57.2	357	18 AAW34331	Tomato yellow leaf
36	199	55.0	357	18 AAW34337	Tomato yellow leaf
37	96	26.5	142	24 ABP58120	Tomato yellow leaf
38	77	21.3	857	23 ABP62804	Protein fragment #
39	70.5	19.5	945	22 ABB65231	Drosophila melanog
40	66.5	18.4	665	22 ABB70391	Drosophila melanog
41	65	18.0	232	21 AAY92317	Geminivirus Rep Cl
42	65	18.0	335	21 AAY92318	Macrotivirus Rep in
43	64.5	17.8	299	18 AAW55450	H. pylori ORF 02ae
44	64.5	17.8	512	19 AAW68473	HIV-1 strain YBF30
45	62.5	17.3	447	21 AAY99659	Human GTPase assoc

ALIGNMENTS

RESULT 1
AAB18685
ID AAB18685 standard; peptide; 70 AA.
XX
AC AAB18685;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 10 /note= "wild type residue replaced with Ala"
XX
FN WO200054573-A1.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-US06759.
XX
PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYN-C) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;

XX DR WPI; 2000-618851/59.

XX XX Transgenic plants with increased resistance to geminivirus infection

XX PT comprise a nucleic acid construct containing a nucleic acid sequence

XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region

XX PT -

XX PS Claim 53; Page 46; 73pp; English.

XX CC The present sequence represents a mutant peptide, derived from a

XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds

XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded

XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1

XX CC protein are used to produce transgenic plants. The mutation in AL1 is

XX CC present in a ribosome binding region, and expression of mutant AL1

XX CC protein imparts increased resistance to geminivirus infection in the

XX CC plant. Mutant AL1 proteins are useful for producing plants having

XX CC increased resistance or reduced sensitivity to a geminivirus such as

XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian

XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper

XX CC virus, cotton leaf curl virus or beet curly top virus.

XX SQ Sequence 70 AA;

Query Match 100.0%; Score 362; DB 21; Length 70;

Best Local Similarity 100.0%; Pred. No. 1.2e-37;

Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Db 1 TLVWGEFQVAGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70

Db 61 DRIFDKTPEP 70

RESULT 2

AAB18677

ID AAB18677 standard; peptide; 70 AA.

XX AC AAB18677;

XX DT 22-JAN-2001 (first entry)

XX DE Peptide fragment from Rep protein of TGMV (amino acids 110-179).

XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX KW ribosome binding region; resistance; geminivirus infection.

XX OS Tomato golden mosaic virus.

XX EN WO200054573-A1.

XX PD 21-SEP-2000.

XX PF 15-MAR-2000; 2000WO-US06759.

XX PR 18-MAR-1999; 99US-0125004.

XX PR 09-APR-1999; 99US-0289346.

XX PA (UYNC-) UNIV NORTH CAROLINA STATE.

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;

XX DR WPI; 2000-618851/59.

XX PT Transgenic plants with increased resistance to geminivirus infection

XX PT comprise a nucleic acid construct containing a nucleic acid sequence

XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region

PT XX Disclosure; Page 18; 73pp; English.

XX PS The present sequence is derived from a geminivirus replication (Rep)

XX CC protein, which is also known as AL1. AL1 binds double-stranded DNA,

XX CC catalyzes cleavage and ligation of single-stranded DNA, and interacts

XX CC with other viral and host proteins. Mutants of the AL1 protein are used

XX CC to produce transgenic plants. The mutation in AL1 is present in a

XX CC ribosome binding region, and expression of mutant AL1 protein imparts

XX CC increased resistance to geminivirus infection in the plant. Mutant AL1

XX CC proteins are useful for producing plants having increased resistance or

XX CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,

XX CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl

XX CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato

XX CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,

XX CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or

XX CC beet curly top virus.

XX SQ Sequence 70 AA;

Query Match 98.3%; Score 356; DB 21; Length 70;

Best Local Similarity 98.6%; Pred. No. 6.6e-37;

Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Db 1 TLVWGEFQVAGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70

Db 61 DRIFDKTPEP 70

RESULT 3

AAB18687

ID AAB18687 standard; peptide; 356 AA.

XX AC AAB18687;

XX DT 22-JAN-2001 (first entry)

XX DE Amino acid sequence of a geminivirus replication protein of TGMV.

XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX KW ribosome binding region; resistance; geminivirus infection.

XX OS Tomato golden mosaic virus.

XX PH Key Location/Qualifiers

XX FT Misc-difference 354

XX FT /note= "unspecified amino acid"

XX PN WO200054573-A1.

XX PD 21-SEP-2000.

XX PF 15-MAR-2000; 2000WO-US06759.

XX PR 18-MAR-1999; 99US-0125004.

XX PR 09-APR-1999; 99US-0289346.

XX PA (UYNC-) UNIV NORTH CAROLINA STATE.

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;

XX DR WPI; 2000-618851/59.

XX PT Transgenic plants with increased resistance to geminivirus infection

XX PT comprise a nucleic acid construct containing a nucleic acid sequence

XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region

PS Disclosure; Page 47-48; 73pp; English.

XX The present sequence represents a geminivirus replication (Rep) protein, which is also known as AL1. AL1 binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the AL1 protein are used to produce transgenic plants. The mutation in AL1 is present in a ribosome binding region, and expression of mutant AL1 protein imparts increased resistance to geminivirus infection in the plant. Mutant AL1 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, African cassava mosaic virus, Indian cassava mosaic virus, yellow mosaic virus, bean golden mosaic virus, squash leaf curl virus, Texas leaf curl virus, beet curly top virus.

XX Sequence 356 AA;

Query Match 98.3%; Score 356; DB 21; Length 356;
 Best Local Similarity 98.6%; Pred. No. 5.1e-36;
 Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLVWGFEQVAGRSARGCGCTSDNDAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60
 |||||
 DB 110 TLVWGFEQVAGRSARGCGCTSDNDAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 169
 |||||

QY 61 DRIFDKTPEP 70
 |||||
 DB 170 DRIFDKTPEP 179
 |||||

RESULT 4
 AAB18688
 ID AAB18688 standard; peptide; 70 AA.
 XX AAB18688;
 AC AAB18688;
 XX 22-JAN-2001 (first entry)
 DT 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 FH Misc-difference 19 /note= "wild type residue replaced with Ala"
 FT Misc-difference 20 /note= "wild type residue replaced with Ala"
 FT Misc-difference 20 /note= "wild type residue replaced with Ala"
 FT Misc-difference 20 /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UTNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region

PS Disclosure; Page 48; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a geminivirus replication (Rep) protein, also known as AL1. AL1 binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the AL1 protein are used to produce transgenic plants. The mutation in AL1 is present in a ribosome binding region, and expression of mutant AL1 protein imparts increased resistance to geminivirus infection in the plant. Mutant AL1 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, African cassava mosaic virus, Indian cassava mosaic virus, yellow mosaic virus, bean golden mosaic virus, squash leaf curl virus, Texas leaf curl virus, beet curly top virus.

XX Sequence 70 AA;

Query Match 95.3%; Score 345; DB 21; Length 70;
 Best Local Similarity 95.7%; Pred. No. 1.6e-35;
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGFEQVAGRSARGCGCTSDNDAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60
 |||||
 DB 1 TLVWGFEQVAGRSARGCGCAASNDAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60
 |||||

QY 61 DRIFDKTPEP 70
 |||||
 DB 61 DRIFDKTPEP 70
 |||||

RESULT 5
 AAB18692
 ID AAB18692 standard; peptide; 70 AA.
 XX AAB18692;
 AC AAB18692;
 XX 22-JAN-2001 (first entry)
 DT 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 FH Misc-difference 66 /note= "wild type residue replaced with Ala"
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UTNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region

PT XX Disclosure; Page 50; 73pp; English.

XX CC The present sequence represents a mutant peptide, derived from a

XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds

XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded

XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1

XX CC protein are used to produce transgenic plants. The mutation in AL1 is

XX CC present in a ribosome binding region, and expression of mutant AL1

XX CC protein imparts increased resistance to geminivirus infection in the

XX CC plant. Mutant AL1 proteins are useful for producing plants having

XX CC increased resistance or reduced sensitivity to a geminivirus such as

XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian

XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper

XX CC virus, cotton leaf curl virus or beet curly top virus.

SQ Sequence 70 AA;

Query Match 95.0%; Score 344; DB 21; Length 70;

Best Local Similarity 95.7%; Pred. No. 2.1e-35;

Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

DB 1 TLVWGEFQVAGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70

DB 61 DRIFDKTPEP 70

RESULT 6

AAB18684

ID AAB18684 standard; peptide; 70 AA.

XX AC AAB18684;

XX DT 22-JAN-2001 (first entry)

XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX KW ribosome binding region; resistance; geminivirus infection.

XX OS Synthetic.

XX OS Tomato golden mosaic virus.

XX FH Key Location/Qualifiers

FT Misc-difference 7 /note= "wild type residue replaced with Ala"

FT Misc-difference 8 /note= "wild type residue replaced with Ala"

FT FT

XX WO200054573-A1.

XX PN

XX PD 21-SEP-2000.

XX PF 15-MAR-2000; 2000WO-US06759.

XX PR 18-MAR-1999; 99US-0125004.

XX PR 09-APR-1999; 99US-0289346.

XX XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX PA Hanley-Bowdoin L, Orozco BM, Kong L;

XX PI WPI; 2000-618851/59.

XX DR Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant AL1 protein with a mutation in the Rb binding region

PT

XX Claim 52; Page 45; 73pp; English.

XX CC The present sequence represents a mutant peptide, derived from a

XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds

XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded

XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1

XX CC protein are used to produce transgenic plants. The mutation in AL1 is

XX CC present in a ribosome binding region, and expression of mutant AL1

XX CC protein imparts increased resistance to geminivirus infection in the

XX CC plant. Mutant AL1 proteins are useful for producing plants having

XX CC increased resistance or reduced sensitivity to a geminivirus such as

XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian

XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper

XX CC virus, cotton leaf curl virus or beet curly top virus.

SQ Sequence 70 AA;

Query Match 94.5%; Score 342; DB 21; Length 70;

Best Local Similarity 95.7%; Pred. No. 3.7e-35;

Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

DB 1 TLVWGEAAVDGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70

DB 61 DRIFDKTPEP 70

RESULT 7

AAB18690

ID AAB18690 standard; peptide; 70 AA.

XX AC AAB18690;

XX DT 22-JAN-2001 (first entry)

XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX KW ribosome binding region; resistance; geminivirus infection.

XX OS Synthetic.

XX OS Tomato golden mosaic virus.

XX FH Key Location/Qualifiers

FT Misc-difference 27 /note= "wild type residue replaced with Ala"

FT Misc-difference 30 /note= "wild type residue replaced with Ala"

FT FT

XX WO200054573-A1.

XX PN

XX PD 21-SEP-2000.

XX PF 15-MAR-2000; 2000WO-US06759.

XX PR 18-MAR-1999; 99US-0125004.

XX PR 09-APR-1999; 99US-0289346.

XX XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX PA Hanley-Bowdoin L, Orozco BM, Kong L;

XX PI WPI; 2000-618851/59.

XX DR Transgenic plants with increased resistance to geminivirus infection

PT

PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 PS Disclosure; Page 49; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 94.5%; Score 342; DB 21; Length 70;
 Best Local Similarity 95.7%; Pred. No. 3.7e-35;
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVAGRSARGGCTSDNDAALNASSKEALQIIRKIPKYLQFPHNLNSNL 60
 DB 1 TLVWGEFQVDSARGGCTSDNDAALNASSKEALQIIRKIPKYLQFPHNLNSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 8
 AAB18678
 ID AAB18678 standard; peptide; 70 AA.
 AC AAB18678;
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 12 /note= "wild type residue replaced with Ala"
 FT Misc-difference 13 /note= "wild type residue replaced with Ala"
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-A1.
 FN
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX

DR WPI; 2000-618851/59.
 XX
 PT Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 XX
 CC Claim 53; Page 42-43; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 94.2%; Score 341; DB 21; Length 70;
 Best Local Similarity 94.3%; Pred. No. 5e-35;
 Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVAGRSARGGCTSDNDAALNASSKEALQIIRKIPKYLQFPHNLNSNL 60
 DB 1 TLVWGEFQVDSARGGCTSDNDAALNASSKEALQIIRKIPKYLQFPHNLNSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 9
 AAB18686
 ID AAB18686 standard; peptide; 70 AA.
 AC AAB18686;
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 24 /note= "wild type residue replaced with Leu"
 FT Misc-difference 25 /note= "wild type residue replaced with Leu"
 FT Misc-difference 26 /note= "wild type residue replaced with Leu"
 FT
 XX WO200054573-A1.
 FN
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.

```

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PS Claim 53; Page 46; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 94.2%; Score 341; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 5e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TLVWGEFVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
DB 1 TLVWGEFVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 10
ID AAB18689
XX AAB18689 standard; peptide; 70 AA.
XX AC AAB18689;
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX FH Key Location/Qualifiers
XX FT Misc-difference 22 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX PN WO200054573-A1.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-US06759.
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX XX

```

```

PA XX (UTNC-) UNIV NORTH CAROLINA STATE.
PI XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PS Disclosure; Page 48-49; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 93.9%; Score 340; DB 21; Length 70;
Best Local Similarity 95.7%; Pred. No. 6.6e-35;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGEFVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
DB 1 TLVWGEFVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 11
ID AAB18680
XX AAB18680 standard; peptide; 70 AA.
XX AC AAB18680;
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX FH Key Location/Qualifiers
XX FT Misc-difference 42 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 43 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 44 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 44 /note= "wild type residue replaced with Ala"
XX PN WO200054573-A1.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-US06759.
XX XX

```

```

PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 52; Page 43-44; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, bean golden mosaic
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 93.4%; Score 338; DB 21; Length 70;
XX Best Local Similarity 94.3%; Pred. No. 1.2e-34;
XX Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 TLVWGFQVAGRSARGCGCQTNDAAAEALNASSKEALQIIREKIPEKYLQFPHNLSNL 60
DB 1 TLVWGFQVAGRSARGCGCQTNDAAAEALNASSKEALQIIREKIPEKYLQFPHNLSNL 60
XX
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
XX
RESULT 12
AAB18691
XX
XX AAB18691 standard; peptide; 70 AA.
XX
XX AAB18691;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 34 /note= "wild type residue replaced with Ala"
XX Misc-difference 35 /note= "wild type residue replaced with Ala"
XX Misc-difference 36 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX
PR 18-MAR-2000; 2000WO-US06759.
PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Disclosure; Page 49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, bean golden mosaic
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 93.4%; Score 338; DB 21; Length 70;
XX Best Local Similarity 94.3%; Pred. No. 1.2e-34;
XX Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 TLVWGFQVAGRSARGCGCQTNDAAAEALNASSKEALQIIREKIPEKYLQFPHNLSNL 60
DB 1 TLVWGFQVAGRSARGCGCQTNDAAAEALNASSKEALQIIREKIPEKYLQFPHNLSNL 60
XX
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
XX
RESULT 13
AAB18681
XX
XX AAB18681 standard; peptide; 70 AA.
XX
XX AAB18681;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 47 /note= "wild type residue replaced with Ala"
XX Misc-difference 48 /note= "wild type residue replaced with Ala"
XX Misc-difference 49 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX

```



```

PN WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX -
XX Claim 52; Page 44; 73pp; English.
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 92.5%; Score 335; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 2.8e-34;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TLVWGEFQVAGRSARGGCGTNDAAAEALNASSKEEALQIREKIPKYLQFHNLSNL 60
DB 1 TLVWGEFQVAGRSARGGCGTNDAAAEALNASSKEEALQIREKIPKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 14
AAB18683
XX AAB18683 standard; peptide; 70 AA.
XX AAB18683;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX Misc-difference 59 /note= "wild type residue replaced with Ala"
XX Misc-difference 61 /note= "wild type residue replaced with Ala"
XX FT

```

```

FT Misc-difference 62 /note= "wild type residue replaced with Ala"
XX WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX -
XX Claim 53; Page 45; 73pp; English.
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 92.3%; Score 334; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 3.8e-34;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TLVWGEFQVAGRSARGGCGTNDAAAEALNASSKEEALQIREKIPKYLQFHNLSNL 60
DB 1 TLVWGEFQVAGRSARGGCGTNDAAAEALNASSKEEALQIREKIPKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 AAFDKTPEP 70
RESULT 15
AAB18682
XX AAB18682 standard; peptide; 70 AA.
XX AAB18682;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX Misc-difference 52
XX FT

```


FT Misc-difference 54 /note= "wild type residue replaced with Ala"
 FT FT Misc-difference 55 /note= "wild type residue replaced with Ala"
 FT FT Misc-difference 55 /note= "wild type residue replaced with Ala"

XX WO200054573-A1.

PN

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYNCL) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

XX comprise a nucleic acid construct containing a nucleic acid sequence

XX encoding a mutant Al1 protein with a mutation in the Rb binding region

XX Claim 53; Page 44-45; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a

XX geminivirus replication (Rep) protein, also known as Al1. Al1 binds

XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded

XX DNA, and interacts with other viral and host proteins. Mutants of the Al1

XX protein are used to produce transgenic plants. The mutation in Al1 is

XX present in a ribosome binding region, and expression of mutant Al1

XX plant imparts increased resistance to geminivirus infection in the

XX plant. Mutant Al1 proteins are useful for producing plants having

XX increased resistance or reduced sensitivity to a geminivirus such as

XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian

XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper

XX virus, cotton leaf curl virus or beet curly top virus.

XX SQ Sequence 70 AA;

Query Match 91.7%; Score 332; DB 21; Length 70;

Best Local Similarity 94.3%; Pred. NO. 6.7e-34;

Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRGCGCQTSNDAAAEALNASSKEALQIIRKIKPEKYLFOFHLNSNL 60

DB 1 TLVWGEFQVAGRGCGCQTSNDAAAEALNASSKEALQIIRKIKPEKYLFOFHLNSNL 60

QY 61 DRIFDKTPEP 70

DB 61 DRIFDKTPEP 70

Search completed: December 23, 2003, 08:56:31

Job time : 32.6667 secs

Db 110 TIWGFQVQDGRGARGGQSSANDSYAKALNADSIESTILKEEQKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70
:|||||

Db 170 ERIFVKVPEP 179

RESULT 2
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838.151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5400
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-46

Query Match 61.3%; Score 222; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 1.7e-20;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGFQVAGRSARGGQTSNDAAEALNASSKEALQIIREKIPEKYLFPQPHNLNSNL 60
:|||||

Db 110 TIWGFQVQDGRGARGGQSSANDSYAKALNADSIESTILKEEQKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70
:|||||

Db 170 ERIFVKVPEP 179

RESULT 3
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul

; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838.151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5400
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-49

Query Match 61.3%; Score 222; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 1.7e-20;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGFQVAGRSARGGQTSNDAAEALNASSKEALQIIREKIPEKYLFPQPHNLNSNL 60
:|||||

Db 110 TIWGFQVQDGRGARGGQSSANDSYAKALNADSIESTILKEEQKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70
:|||||

Db 170 ERIFVKVPEP 179

RESULT 4
US-08-838-151A-52
; Sequence 52, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-52

Query Match      61.3%; Score 222; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 1.7e-20;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLVWGEFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db      110 TLWGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFVKVPEP 179

RESULT 5
US-08-838-151A-55
; Sequence 55, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; PRIOR APPLICATION DATA:
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-2

Query Match      61.3%; Score 222; DB 3; Length 359;
Best Local Similarity 58.0%; Pred. No. 1.7e-20;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy      2 LVWGEFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 61
Db      111 LWTGTFQIDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 170
Qy      62 RIFDKTPEP 70
Db      171 ERIFVKVPEP 179
```

```
;
; MOLECULE TYPE: protein
; US-08-838-151A-55

Query Match      61.3%; Score 222; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 1.7e-20;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLVWGEFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db      110 TLWGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFVKVPEP 179

RESULT 6
US-08-809-103B-2
; Sequence 2, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-2

Query Match      61.3%; Score 222; DB 3; Length 359;
Best Local Similarity 58.0%; Pred. No. 1.7e-20;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy      2 LVWGEFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 61
Db      111 LWTGTFQIDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 170
Qy      62 RIFDKTPEP 70
Db      171 ERIFVKVPEP 179
```

Db 171 KVFQVPPAP 179

RESULT 7

US-08-809-103B-4
; Sequence 4, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-4

Query Match 61.3%; Score 222; DB 3; Length 359;

Best Local Similarity 58.0%; Pred. No. 1.7e-20;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 LVWGFQVAGRSARGCOTSNDAAAEALNASSKEALQIREKIPKYLFOFHNLNSLD 61
Db 111 LEMGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFHNLNSLD 170
QY 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 8

US-08-809-103B-6
; Sequence 6, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-6

Query Match 61.3%; Score 222; DB 3; Length 359;

Best Local Similarity 58.0%; Pred. No. 1.7e-20;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 LVWGFQVAGRSARGCOTSNDAAAEALNASSKEALQIREKIPKYLFOFHNLNSLD 61
Db 111 LEMGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFHNLNSLD 170
QY 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 9

US-08-809-103B-8
; Sequence 8, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:

; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B

```
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8

Query Match 61.3%; Score 222; DB 3; Length 359;
Best Local Similarity 58.0%; Pred. No. 1.7e-20;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 LVNGEFQVAGRSARGGCGTSDNDAALNASSKEEALQIIRKIPKYLQFHNLSNLD 61
Db 111 LEWGTFOIDGRSARGGCGTNDAYAKAINAGSKQALDYIKELAPRDYVLHFNINSNLD 170

QY 62 RIFDKTPEP 70
Db 171 KVFOVPPAP 179

RESULT 10
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match 60.8%; Score 220; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 3.1e-20;
Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVNGEFQVAGRSARGGCGTSDNDAALNASSKEEALQIIRKIPKYLQFHNLSNLD 60
Db 110 TIWGDFOIDGRSARGGCGQSANDSYAKALNASSVQSALAVLRBEPQKDFVLQNHINRSNLD 169

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-2

Query Match 60.8%; Score 220; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 3.1e-20;
Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVNGEFQVAGRSARGGCGTSDNDAALNASSKEEALQIIRKIPKYLQFHNLSNLD 60
Db 110 TIWGDFOIDGRSARGGCGQSANDSYAKALNASSVQSALAVLRBEPQKDFVLQNHINRSNLD 169
```

[illegible]

```
;
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-24

Query Match          57.2%; Score 207; DB 3; Length 357;
Best Local Similarity 65.6%; Pred.No. 1.5e-18;
Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY      4 WGEFQVAGRSARGGCGQTSNDAAAEALNASKEEALQIIREKIPKYLFPQFHNLSNLDRI 63
Db      111 FGVSDIGRSARGGQGSANDAYAEALNSGSKSEALNLIKKEAPKDYILQFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

US-08-838-151A-27

Query Match          57.2%; Score 207; DB 3; Length 357;
Best Local Similarity 65.6%; Pred.No. 1.5e-18;
Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY      4 WGEFQVAGRSARGGCGQTSNDAAAEALNASKEEALQIIREKIPKYLFPQFHNLSNLDRI 63
Db      111 FGVSDIGRSARGGQGSANDAYAEALNSGSKSEALNLIKKEAPKDYILQFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

US-08-838-151A-27

RESULT 15
US-08-838-151A-27
; Sequence 27, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-27
```

```
Query Match          57.2%; Score 207; DB 3; Length 357;
Best Local Similarity 65.6%; Pred.No. 1.5e-18;
Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY      4 WGEFQVAGRSARGGCGQTSNDAAAEALNASKEEALQIIREKIPKYLFPQFHNLSNLDRI 63
Db      111 FGVSDIGRSARGGQGSANDAYAEALNSGSKSEALNLIKKEAPKDYILQFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

Search completed: December 23, 2003, 08:59:35
Job time : 11.6667 secs
```



```
Db          61 DRIFDKTPEP 70
|||||
RESULT 2
US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1
Query Match      98.3%; Score 356; DB 10; Length 70;
Best Local Similarity 98.6%; Pred. No. 4.8e-38;
Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
|||||
RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11
Query Match      98.3%; Score 356; DB 10; Length 356;
Best Local Similarity 98.6%; Pred. No. 4e-37;
Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
|||||
```

```
Db          110 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 169
QY          61 DRIFDKTPEP 70
|||||
Db          170 DRIFDKTPEP 179
|||||
RESULT 4
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12
Query Match      95.3%; Score 345; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 1.2e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
|||||
RESULT 5
US-09-289-346A-16
; Sequence 16, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-16
Query Match      95.0%; Score 344; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 1.7e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
```

```

QY      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

RESULT 6
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->M118).
US-09-289-346A-8

Query Match      94.5%; Score 342; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 3e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TLVWGEFQVAGRSARGGCGTSDNDAALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db      1 TLVWGERAVDGRSARGGCGTSDNDAALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

RESULT 7
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match      94.5%; Score 342; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 3e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

RESULT 8
US-09-289-346A-2
; Sequence 2, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
US-09-289-346A-2

Query Match      94.2%; Score 341; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 4e-36;
Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 TLVWGEFQVAGRSARGGCGTSDNDAALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db      1 TLVWGEFQVAGRSARGGCGTSDNDAALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

RESULT 9
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-10

Query Match      94.2%; Score 341; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 4e-36;
Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 TLVWGEFQVAGRSARGGCGTSDNDAALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db      1 TLVWGEFQVAGRSARGGCGTSDNDAALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

```

Tue Dec 23 09:55:39 2003

```
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)...(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAAL36->LLU136).
US-09-289-346A-10

Query Match          94.2%; Score 341; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 4e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
   |||||
Db 1 TLVWGEFQVAGRSARGCGCOTSDNDLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-13

Query Match          93.9%; Score 340; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 5.4e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
   |||||
Db 1 TLVWGEFQVAGRSARGCGCOTSDNAAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18

; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-4

Query Match          93.4%; Score 338; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 9.7e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
   |||||
Db 1 TLVWGEFQVAGRSARGCGCOTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match          93.4%; Score 338; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 9.7e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
   |||||
Db 1 TLVWGEFQVAGRSARGCGCOTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: 60/125,004
; PRIOR APPLICATION NUMBER: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-5

Query Match          93.4%; Score 338; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 9.7e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
   |||||
Db 1 TLVWGEFQVAGRSARGCGCOTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
```

```

RESULT 15
US-09-289-346A-6
; Sequence 6, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Grulasesm, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURES:
; NAME/KEY: VARIANT
; LOCATION: (52)..(55)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (QPHN165->AFAA165).
US-09-289-346A-6

Query Match          91.7%; Score 332; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 5.7e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TLVWGSEFQVAGRSARGCQTSNDAAAEALNASSKEEALQIIRKIPKYLQPHNLSNL 60
    |||||
Db 1 TLVWGSEFQVAGRSARGCQTSNDAAAEALNASSKEEALQIIRKIPKYLQPHNLSNL 60
    |||||

Qy 61 DRIFDKTPEP 70
    |||||
Db 61 DRIFDKTPEP 70
    |||||

Search completed: December 23, 2003, 09:43:31
Job time : 76 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds
(without alignments)
673.181 Million cell updates/sec

Title: US-09-289-346B-9

Perfect score: 362

Sequence: 1 TLVWGSEFQVAGRSARGCQT.....FQFHNLNMLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	356	98.3	352	1 CQCVL1	Al1 protein - toma
2	256	70.7	361	1 CQCVT	Al1 protein - toma
3	243	67.1	358	2 S07S94	hypothetical prote
4	236	65.2	362	1 JQ1887	Al1 protein - toma
5	229	63.3	359	2 S39211	gene C1 protein -
6	225	62.2	349	2 JQ2300	replicase - pepp
7	225	62.2	349	2 S31875	Al1 protein - pepp
8	222	61.3	359	2 S22593	hypothetical prote
9	219	60.5	351	2 JQ2327	Al1 protein - Indi
10	219	60.5	355	1 CQCVM1	AV1 protein - abut
11	216	59.7	358	1 JQ1870	Al1 protein - toma
12	216	59.7	359	2 S39235	gene C1 protein -
13	216	59.7	385	2 S28360	Al1 protein - beet
14	209	57.7	360	2 S59885	replication-associ
15	207	57.2	357	1 CQCVC1	Al1 protein - toma
16	142	39.2	131	2 S45059	AC1 protein (clone
17	125	34.5	347	1 CQCVS1	Al1 protein - squa
18	68	18.8	587	2 UC1439	Pc gamma (IgG) rec
19	67	18.5	840	2 T36175	probable large ATP
20	64.5	17.8	299	2 B71967	probable peptidyl-
21	63.5	17.5	642	2 D90558	topoisomerase iv s
22	63	17.4	714	2 C95382	probable ferrichro
23	62.5	17.3	447	2 T12544	hypothetical prote
24	62	17.1	154	2 AD3475	protein-Npi-phosph
25	62	17.1	181	2 G37976	conserved hypochet
26	62	17.1	295	2 D42452	C1 protein - tobac
27	62	17.1	340	2 B97011	probably O-sialogl
28	61.5	17.0	201	2 A81380	probable flagellar
29	61.5	17.0	481	2 A70091	probable phosphoes

30	61	16.9	1502	1 RGVH11	CYC1/CYP3 tranacri
31	60.5	16.7	1713	2 AS5347	adhesive ligand ep
32	60.5	16.7	2137	2 T05244	hypothetical prote
33	60	16.6	160	2 G82060	hypothetical prote
34	60	16.6	319	2 B90067	L-lactate dehydrog
35	60	16.6	447	2 S52437	CDP-diacylglycerol
36	60	16.6	988	2 P86316	protein T10022.13
37	59.5	16.4	1033	2 E97700	hypothetical prote
38	59	16.3	338	2 AG3582	iron(III)-binding
39	59	16.3	337	2 B71078	probable NADH oxid
40	59	16.3	416	2 A82892	hypothetical prote
41	59	16.3	862	2 H82182	conserved hypochet
42	59	16.3	1287	2 S55954	viral mRNA transla
43	59	16.3	1341	2 JG0166	lamDRI protein - L
44	58.5	16.2	180	2 D84082	hypothetical prote
45	58.5	16.2	230	2 S46332	homeotic protein G

ALIGNMENTS

RESULT 1

CQCVL1

Al1 protein - tomato golden mosaic virus

C:Species: tomato golden mosaic virus

A:Note: host Nicotiana sp. (tobacco)

C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994

C:Accession: A04170

R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.

EMBO J. 3, 2197-2205, 1984

A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat

A:Reference number: A04163

A:Accession: A04170

A:Molecule type: DNA

A:Residues: 1-352 <HAM>

C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A

C:Genetics:

A:Map position: segment A

C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 98.3%; Score 356; DB 1; Length 352;
Best Local Similarity 98.6%; Pred. No. 1.7e-32;
Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLVWGSEFQVAGRSARGCQTSDNAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60

DB 111 TLVWGSEFQVAGRSARGCQTSDNAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 170

QY 61 DRIFDKTPEP 70

DB 171 DRIFDKTPEP 180

RESULT 2

CQCVT

Al1 protein - potato yellow mosaic virus (isolate Venezuela)

C:Species: potato yellow mosaic virus

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000

C:Accession: J00364

R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.

J. Gen. Virol. 72, 1515-1520, 1991

A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel

A:Reference number: J00362; MUID:91311403; PMID:1856690

A:Accession: J00364

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-361 <COU>

A:Cross-references: GB:D00940; NID:G222458; PIDN:BAA00782.1; PID:G222459

C:Genetics:

A:Map position: segment A

C:Superfamily: tomato golden mosaic virus Al1 protein

A:Accession: S31875

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 <TOR>

A:Cross-references: EMBL:X70418; NID:G61023; PIDN:CAA49856.1; PID:G61025

A>Note: the source is designated as pepper huasteco virus

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 62.2%; Score 225; DB 2; Length 349;

Best Local Similarity 60.0%; Pred. No. 1.1e-17; Indels 0; Gaps 0;

Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNLD 60

Db 110 TVEWGFQIDGRSARGCGQANDYAKALNSAEALQIIREKPEQHFQHFQHNIVSNA 169

Qy 61 DRFDKTPPEP 70

Db 170 NRIFQTPPEP 179

RESULT 8

S22593

hypothetical protein C4 - tomato yellow leaf curl virus

C:Species: tomato yellow leaf curl virus

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999

C:Accession: S22593

R:Kheyr-Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.

Nucleic Acids Res. 19, 6763-6769, 1991

A:Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite

A:Reference number: S22588; MUID:92107660; PMID:1840676

A:Accession: S22593

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-359 <RHE>

A:Cross-references: EMBL:X61153; NID:G62211; PIDN:CAA43466.1; PID:G62217

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 61.3%; Score 222; DB 2; Length 359;

Best Local Similarity 58.0%; Pred. No. 2.4e-17; Indels 0; Gaps 0;

Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 2 LVWGFQVAGRSARGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNLD 61

Db 111 LEWCTFQIDGRSARGCGQANDYAKALNSAEALQIIREKPEQHFQHFQHNIVSNA 170

Qy 62 RFDKTPPEP 70

Db 171 KVQVPPAP 179

RESULT 9

JQ2327

AL1 protein - Indian caseava mosaic virus

C:Species: Indian caseava mosaic virus

C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 20-Sep-1999

C:Accession: JQ2327; S35883

R:Hong, Y.G.; Robinson, D.J.; Harrison, B.D.

J. Gen. Virol. 74, 2437-2443, 1993

A:Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-trans

A:Reference number: JQ2326; MUID:94065670; PMID:8245859

A:Accession: JQ2327

A:Molecule type: DNA

A:Residues: 1-351 <HON>

A:Cross-references: EMBL:Z24758; NID:G395351; PIDN:CAA80891.1; PID:G584046

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match

Best Local Similarity 60.5%; Score 219; DB 2; Length 351;

Matches 42; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 4 WGEFQVAGRSARGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNLDRI 63

Db 113 MGTQFQIDGRSARGCGQANDYAKALNSAEALQIIREKPEQHFQHFQHNIVSNA 172

Qy 64 FDKTPPEP 70

Db 173 FTKPPPP 179

RESULT 10

QOCVW1

AV1 protein - abutilon mosaic virus (isolate West India)

C:Species: abutilon mosaic virus

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Apr-1994

C:Accession: A36214

R:Frischmuth, T.; Zimmat, G.; Jeske, H.

Virol. 178, 461-468, 1990

A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as w

A:Reference number: A36214; MUID:91020984; PMID:2219703

A:Accession: A36214

A:Molecule type: DNA

A:Residues: 1-355 <FRI>

A:Cross-references: EMBL:X15983

C:Genetics:

A:Map position: segment A

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 60.5%; Score 219; DB 1; Length 355;

Best Local Similarity 58.6%; Pred. No. 5.2e-17;

Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNLD 60

Db 110 TAEWGFQIDGRSARGCGQANDYAKALNSAEALQIIREKPEQHFQHFQHNIVSNA 169

Qy 61 DRFDKTPPEP 70

Db 170 ERIFAKAPEP 179

RESULT 11

JQ1870

AL1 protein - tomato mottle virus (isolate Florida)

C:Species: tomato mottle virus

C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999

C:Accession: JQ1870

R:Abouzid, A.M.; Poleston, J.E.; Hiebert, E.

J. Gen. Virol. 73, 3225-3229, 1992

A:Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated fr

A:Reference number: JQ1869; MUID:93107858; PMID:1469361

A:Accession: JQ1870

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-358 <ABO>

A:Cross-references: GB:L14460

C:Genetics:

A:Map position: segment A

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.7%; Score 216; DB 1; Length 358;

Best Local Similarity 55.7%; Pred. No. 1.2e-16;

Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNLD 60

Db 107 TIWGFQIDGRSARGCGQANDYAKALNSAEALQIIREKPEQHFQHFQHNIVSNA 166

Qy 61 DRFDKTPPEP 70

Db 167 ERIFAKAPEP 176

RESULT 12

S39235

Gene C1 protein - tomato yellow leaf curl virus
 C:Species: tomato yellow leaf curl virus
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
 C:Accession: S39235
 R:Crepi, S.; Norris, E.; Vaira, A.; Bosco, D.; Accotto, G.
 submitted to the EMBL Data Library, December 1993
 A:Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.
 A:Reference number: S39233
 A:Accession: S39235
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-359 <CR>
 A:Cross-references: EMBL:Z28390; NID:g1041671; PID:gl334964
 C:Superfamily: tomato golden mosaic virus All protein

Query Match 59.7%; Score 216; DB 2; Length 359;
 Best Local Similarity 56.5%; Pred. No. 1.2e-16;
 Matches 39; Conservative 12; Mismatches 18; Indels 0; Gaps 0;
 QY 2 LWGEFQVAGRSARGGCGTSDNDAAEALNASSKEALQIREKIPEKYLQFHNLSNLD 61
 DB 111 LEWTFQIDGRSARGGCGQTANDAYAKALNASKSEALDVIKLAPRDYVLHFNHNSNLD 170
 QY 62 RIFDKTPPEP 70
 DB 171 KVFQVPPAP 179

RESULT 13

S28360
 All protein - beet curly top virus
 C:Species: beet curly top virus
 C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Sep-1999
 C:Accession: S28360
 R:Stanley, J.; Markham, P.G.; Callis, R.J.; Pinner, M.S.
 EMBL J. 5, 1761-1767, 1986
 A:Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly top virus
 A:Reference number: S28360
 A:Accession: S28360
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-385 <STR>
 A:Cross-references: GB:M24597; EMBL:X04144; NID:g210678; PIDN:AAA42751.1; PID:g210679
 C:Superfamily: tomato golden mosaic virus All protein

Query Match 59.7%; Score 216; DB 2; Length 385;
 Best Local Similarity 55.7%; Pred. No. 1.3e-16;
 Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;
 QY 1 TLVWGEFQVAGRSARGGCGTSDNDAAEALNASSKEALQIREKIPEKYLQFHNLSNLD 60
 DB 137 TIWGEFQIDGRSARGGCGQTANDSYAKALNATSLDQALQIIEKPEQPKDYFLQHNLLNA 196
 QY 61 DRIFDKTPPEP 70
 DB 197 QKIFQRPDP 206

RESULT 14

S59885
 replication-associated protein C1 - tomato yellow leaf curl virus
 C:Species: tomato yellow leaf curl virus
 C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
 C:Accession: S59885
 R:Hong, Y.; Harrison, B.D.
 submitted to the EMBL Data Library, February 1995
 A:Description: Nucleotide sequences from tomato leaf curl viruses from different countries
 A:Reference number: S58346
 A:Accession: S59885
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-360 <HON>

A:Cross-references: EMBL:Z48182; NID:g944838; PIDN:CAA88229.1; PID:g974211
 C:Superfamily: tomato golden mosaic virus All protein

Query Match 57.7%; Score 209; DB 2; Length 360;
 Best Local Similarity 60.6%; Pred. No. 7.2e-16;
 Matches 40; Conservative 12; Mismatches 14; Indels 0; Gaps 0;
 QY 4 WGEFQVAGRSARGGCGTSDNDAAEALNASSKEALQIREKIPEKYLQFHNLSNLDRI 63
 DB 113 FGVFQIDGRSARGGCGQSANDAYAEALNSGSAALDILREKAPKDFVLQFHNLSNLDRI 172
 QY 64 FDKTPPEP 69
 DB 173 FTFPSAE 178

RESULT 15

QCCVCI
 All protein - tomato yellow leaf curl virus
 N:Alternate names: C1 protein
 C:Species: tomato yellow leaf curl virus
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
 C:Accession: D40779
 R:Navot, N.; Fichersky, B.; Zeidan, M.; Zamir, D.; Czosnek, H.
 Virology 185, 151-161, 1991
 A:Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single ORF
 A:Reference number: A40779; MUID:92024070; PMID:1926771
 A:Accession: D40779
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-357 <NAV>
 A:Cross-references: GB:X15656; NID:g62204; PIDN:CAA33688.1; PID:g62207
 C:Superfamily: tomato golden mosaic virus All protein

Query Match 57.2%; Score 207; DB 1; Length 357;
 Best Local Similarity 65.6%; Pred. No. 1.2e-15;
 Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 4 WGEFQVAGRSARGGCGTSDNDAAEALNASSKEALQIREKIPEKYLQFHNLSNLDRI 63
 DB 111 FGVFQIDGRSARGGCGQSANDAYAEALNSGSAALDILREKAPKDFVLQFHNLSNLDRI 170
 QY 64 F 64
 DB 171 F 171

Search completed: December 23, 2003, 09:05:24
 Job time : 11 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds
(without alignments)
569.747 Million cell updates/sec

Title: US-09-289-346B-9

Perfect score: 362

Sequence: 1 TLVWGFQVAGRSARGGQCT.....FOFHNLNSLDRIFDKTEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	356	98.3	352	1 VAL1_TGMV	P03567 tomato gold
2	256	70.7	361	1 VAL1_PYMV	P27258 potato yell
3	243	67.1	358	1 VAL1_CLVK	P14982 cassava lat
4	243	67.1	358	1 VAL1_CLVN	P14972 cassava lat
5	236	65.2	362	1 VAL1_TYLC	P36279 tomato yell
6	229	63.3	359	1 VAL1_TYLCU	P38609 tomato yell
7	225	62.2	349	1 VAL1_PHVU	P06523 pepper huas
8	222	61.3	359	1 VAL1_TYLCM	P27260 tomato yell
9	220	60.8	353	1 VAL1_BGMV	P05175 bean golden
10	219	60.5	355	1 VAL1_ABMVW	P21947 abutilon mo
11	216	59.7	358	1 VAL1_BCTV	P14991 beet curly
12	216	59.7	361	1 VAL1_TMOV	P06657 tomato molt
13	207	57.2	357	1 VAL1_TYLCV	P27359 tomato yell
14	125	34.5	347	1 VAL1_SLVC	P29048 squash leaf
15	65.5	18.1	298	1 OUG2_CHICK	P90363 gallus gall
16	64.5	17.8	299	1 Y175_HELPJ	P92407 helicobacte
17	62.5	17.3	447	1 TBL2_HUMAN	P94423 homo sapien
18	62	17.1	295	1 VAL1_TYDVA	P31617 tobacco vel
19	61	16.9	1502	1 CVP1_YEAST	P12351 saccharomyc
20	60.5	16.7	259	1 FLGH_VIRVU	P08651 vibrio vuln
21	60.5	16.7	1713	1 LMA3_HUMAN	P12351 homo sapien
22	60	16.6	319	1 LDH2_STAAM	P99735 staphylococ
23	60	16.6	319	1 LDH2_STAAM	P99735 staphylococ
24	60	16.6	447	1 CDS4_DROME	P56079 d phosphati
25	60	16.6	719	1 CAT3_NEUCR	P94169 neurospora
26	59.5	16.4	476	1 DGR2_HUMAN	P96df8 homo sapien
27	59.5	16.4	479	1 DGR2_MOUSE	P70279 mus musculu
28	59	16.3	1287	1 SK12_YEAST	P35207 saccharomyc
29	58.5	16.2	297	1 RKP2_RABVP	P06747 rabies viru
30	58.5	16.2	299	1 Y175_HELPJ	P56112 helicobacte
31	58.5	16.2	367	1 LHX4_MOUSE	P53776 mus musculu
32	58.5	16.2	491	1 AMPA_ANASP	P82064 anabaena sp
33	58.5	16.2	589	1 YB67_HABIN	P45221 haemophilus

34 58.5 16.2 1044 1 RUB1_SCHPO
35 58 16.0 207 1 IL6_MARMO
36 58 16.0 256 1 UT11_YEAST
37 58 16.0 617 1 YACH_ECOLI
38 58 16.0 874 1 SLAP_BACLI
39 57.5 15.9 136 1 Y452_CABEL
40 57 15.7 355 1 CRTB_RHOSH
41 57 15.7 492 1 MOT3_MOUSE
42 57 15.7 492 1 MOT3_RAT
43 56.5 15.6 428 1 GBA1_CANAL
44 56.5 15.6 470 1 RBA1_RHIME
45 56.5 15.6 487 1 DLTA_STAXY

ALIGNMENTS

RESULT 1

VAL1_TGMV STANDARD; PRT; 352 AA.

AC P03567;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE ALL protein.

GN ACl.

OS Tomato golden mosaic virus (TGMV).

OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

OX NCBI_TaxID=10831;

RN [1]

RP SEQUENCE FROM N.A.

RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;

RT "Complete nucleotide sequence of the infectious cloned DNA components

of tomato golden mosaic virus: potential coding regions and regulatory

sequences.";

RL EMBO J. 3:2197-2205(1984).

CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; K02029; -; NOT ANNOTATED CDS.

DR PIR; A04170; QCCVLI.

DR InterPro; IPR001191; Gemini_All.

DR Pfam; PF00799; Gemini_All; 1.

DR PRINTS; PR00227; GEMCOATALL.

DR ProDom; PD000736; Gemini_All; 1.

KW ATP-binding. 223 230 ATP (POTENTIAL).

FT NP_BIND 223 230

SQ SEQUENCE 352 AA; 40332 MW; C33C938B9644B4A4 CRC64;

Query Match

Best Local Similarity 98.3%; Score 356; DB 1; Length 352;

Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLVWGFQVAGRSARGGCGTSDNAAALNASSKEALQIIRKPKYLPQFNLNSNL 60

DB 111 TLVWGFQVDRSARGGCGTSDNAAALNASSKEALQIIRKPKYLPQFNLNSNL 170

QY 61 DRIFDKTEP 70

DB 171 DRIFDKTEP 180

RESULT 2

VAL1_PYMV

ID VAL1_PYMV STANDARD; PRT; 361 AA.

AC P27258;

```

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE A11 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D00940; BAA0782.1; -
DR PIR; J00364; QQCVP.
DR InterPro; IPR001191; Gemini_A11.
DR Pfam; PF00799; Gemini_A11; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_A11; 1.
DR ATP-binding.
KW NP-BIND.
FT NP-BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;
Query Match 70.7%; Score 256; DB 1; Length 361;
Best Local Similarity 69.6%; Pred. No. 3.3e-21;
Matches 48; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
QY 1 TLVWGEFQVAGSRGGCGQTNDAAALNASSKEALQIIRKIPKYLQFHNLSNL 60
Db 110 TIWGLFQIDGSRGGCGQTNDAAALNASSKEALQIIRKIPKYLQFHNLSNL 169
QY 61 DRIFDKTPE 69
Db 170 DRIFWKAPE 178
RESULT 3
VAL1_CLVK
ID VAL1 CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE A11 protein (40.4 kDa protein).
GN ACl.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX Stanley J., Gay M.R.;
RA "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

```

CC EMBL; J02057; -, NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_A11.
DR Pfam; PF00799; Gemini_A11; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_A11; 1.
KW ATP-binding.
FT NP-BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753EE92D69 CRC64;
Query Match 67.1%; Score 243; DB 1; Length 358;
Best Local Similarity 62.9%; Pred. No. 9.1e-20;
Matches 44; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
QY 1 TLVWGEFQVAGSRGGCGQTNDAAALNASSKEALQIIRKIPKYLQFHNLSNL 60
Db 109 TVEWQFQIDGSRGGCGQTNDAAALNASSKEALQIIRKIPKYLQFHNLSNL 169
QY 61 DRIFDKTPE 70
Db 169 DRIFOEPPAP 178
RESULT 4
VAL1_CLVN
ID VAL1 CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE A11 protein (40.4 kDa protein).
GN ACl.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain)."
RL Nucleic Acids Res. 18:197-198(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X17095; CAA34953.1; -
DR PIR; S07594; S07594.
DR InterPro; IPR001191; Gemini_A11.
DR Pfam; PF00799; Gemini_A11; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_A11; 1.
KW ATP-binding.
FT NP-BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16BB0CB2D5E2C CRC64;
Query Match 67.1%; Score 243; DB 1; Length 358;
Best Local Similarity 62.9%; Pred. No. 9.1e-20;
Matches 44; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
QY 1 TLVWGEFQVAGSRGGCGQTNDAAALNASSKEALQIIRKIPKYLQFHNLSNL 60
Db 109 TVEWQFQIDGSRGGCGQTNDAAALNASSKEALQIIRKIPKYLQFHNLSNL 168
QY 61 DRIFDKTPE 70
Db 169 DRIFOEPPAP 178

```

```

RESULT 5
VAL1_TYLCU
ID VAL1_TYLCU STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AL1 protein (C1 protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Rigden J.E., Krake L.R., Mullineaux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
geminivirus."
RL J. Gen. Virol. 74:147-151(1993).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR PIR; JQ1887; JQ1887.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 65.2%; Score 236; DB 1; Length 362;
Best Local Similarity 55.3%; Pred. No. 5.6e-19;
Matches 47; Conservative 9; Mismatches 13; Indels 16; Gaps 1;

Qy 1 TLVGFQVAGRSARGCGQTSNDAAAEALNASSKEALQIIREKIPEKYLQFPHNLNSNL 60
Db 110 TLEWGFQIDGRSARGGQQTANDAYAKAINAGSKSEALDVIKELAPROYILFFHNLNSLD 170

Qy 61 DRI-----FDKTPK 69
Db 170 DRIPTPELVVSPFLSSSPDRVPE 194

RESULT 6
VAL1_TYLCU
ID VAL1_TYLCU STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (C1 protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Noris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
from the west Mediterranean basin: the nucleotide sequence of an
RT infectious clone from Spain."
RL Arch. Virol. 135:165-170(1994).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC Query Match 62.2%; Score 225; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 9.1e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVGFQVAGRSARGCGQTSNDAAAEALNASSKEALQIIREKIPEKYLQFPHNLNSNL 60
Db 110 TVEWGFQIDGRSARGGQQTANDAYAKAINAGSKSEALDVIKELAPROYILFFHNLNSLD 169

```

61 DRIEDKTPPEP 70
:|||||
170 NRIFQTPPEP 179

ULT 8
JL TYLCM
1 VAL1 TYLCM STANDARD; PRT; 359 AA.
P27260;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Al1 protein (Cl protein).
Cl.
Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=10833;
[1]
SEQUENCE FROM N.A.
MEDLINE=92107660; PubMed=1840676;
A Kheyr-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
A Gronenborn B.; leaf curl virus from Sardinia is a
T whitefly-transmitted monopartite Geminivirus.;
L Nucleic Acids Res. 19:6763-6769(1991).
C -/- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
C
C This SWISS-PROT entry is copyright. It is produced through a collaboration
C between the Swiss Institute of Bioinformatics and the EMBL outstation -
C the European Bioinformatics Institute. There are no restrictions on its
C use by non-profit institutions as long as its content is in no way
C modified and this statement is not removed. Usage by and for commercial
C entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
C or send an email to license@isb-sib.ch).
C
C EMBL; M10070; AAA46318.1; -;
C InterPro; IPR001191; Gemini_AL1.
C Pfam; PF00799; Gemini_AL1; 1.
C PRINTS; PR00227; GEMCOATALL.
C ProDom; PD000736; Gemini_AL1; 1.
C ATP-binding. 222 229 ATP (POTENTIAL).
C NP BIND 353 AA; 40130 MW; 80FA77DF6029A34 CRC64;
C SEQUENCE 353 AA; 40130 MW; 80FA77DF6029A34 CRC64;
C
C Query Match 60.8%; Score 220; DB 1; Length 353;
C Best Local Similarity 60.0%; Pred. No. 3.e-17;
C Matches 40; Conservative 11; Mismatches 16; Indels 0; Gaps 0;
C
C QY 1 LVWGTFQVAGRSARGGCGTNDAAAPALNASSKEALQIIREKIPKYLFOFHNLSNLD 61
C Db 110 TIEMGQFQVDSARGGCGTNDAAAPALNASSKEALQIIREKIPKYLFOFHNLSNLD 169
C
C QY 61 DRIEDKTPPEP 70
C Db 170 NRIFQTPPEP 179

RESULT 10
VAL1 ABMVW STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN ACL.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimmat G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features."
RL Virology 178:461-468(1990).
CC -/- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X15983; -; NOT ANNOTATED_CDS.
C
C PIR; A36214; QOCVW1.
C InterPro; IPR001191; Gemini_AL1.
C Pfam; PF00799; Gemini_AL1; 1.
C PRINTS; PR00227; GEMCOATALL.
C ProDom; PD000736; Gemini_AL1; 1.
C ATP-binding.
C
C QY 2 LVWGTFQVAGRSARGGCGTNDAAAPALNASSKEALQIIREKIPKYLFOFHNLSNLD 61
C Db 111 LEWGTQVDSARGGCGTNDAAAPALNASSKEALQIIREKIPKYLFOFHNLSNLD 170
C
C QY 62 RIFDKTPPEP 70
C Db 171 KVQVPPAP 179

RESULT 9
VAL1 BGWV STANDARD; PRT; 353 AA.
AC F05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE AL1 protein (40.2 kDa protein).
GN ACL.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]

```

FT NP BIND 221 228 ATP (POTENTIAL)
SQ SEQUENCE 355 AA; 40257 MW; 16A2CAGA63251E95 CRC64;

Query Match 60.5%; Score 219; DB 1; Length 355;
Best Local Similarity 58.6%; Pred. No. 4.3e-17;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVGEFQVAGRGAGCGQTSNDAAAEALNASSKEEALQIREKIPKYLQFPHNLNSL 60
DB 110 TAEGEFQIDGRSARGGQQTANDSYAKALNAGVQSAALNLKEEQPKDYVLQHNIRSL 169
QY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 11
VAL1 BCTV STANDARD; PRT; 358 AA.
AC P14951;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
beet curly top virus."
RL EMBO J. 5:1761-1767(1986).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; L14460; AAC32414.1; -
PIR; JQ1870; JQ1870.
InterPro; IPR001191; Gemini_AL1.
Pfam; PF00799; Gemini_AL1; 1.
PRINTS; PR00227; GEMCOATALI.
ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
NP_BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match 59.7%; Score 216; DB 1; Length 358;
Best Local Similarity 55.7%; Pred. No. 9.5e-17;
Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVGEFQVAGRGAGCGQTSNDAAAEALNASSKEEALQIREKIPKYLQFPHNLNSL 60
DB 110 TIEWGEFQIDGRSARGGQQTANDSYAKALNAGVQSAALNLKEEQPKDYVLQHNIRSL 169
QY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 12
VAL1 TMOV STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; X04144; -; NOT ANNOTATED CDS.
InterPro; IPR001191; Gemini_AL1.
Pfam; PF00799; Gemini_AL1; 1.
PRINTS; PR00227; GEMCOATALI.
ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
NP_BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match 59.7%; Score 216; DB 1; Length 358;
Best Local Similarity 55.7%; Pred. No. 9.5e-17;
Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVGEFQVAGRGAGCGQTSNDAAAEALNASSKEEALQIREKIPKYLQFPHNLNSL 60
DB 110 TIEWGEFQIDGRSARGGQQTANDSYAKALNAGVQSAALNLKEEQPKDYVLQHNIRSL 169
QY 61 DRIFDKTPEP 70
DB 170 QKIFORPPDP 179

RESULT 13
VAL1 TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (C1 protein).
GN C1
OS Tomato yellow leaf curl virus (TYLCV). Begomovirus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
with a single genomic component."
RL Virology 185:151-161(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

```

```
DR EMBL; X15656; CAA33688.1; -.
DR PIR; D40779; QOCVCI.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1.1.
DR ATP-binding. 219 226 ATP (POTENTIAL).
KW NP_BIND 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match 57.2%; Score 207; DB 1; Length 357;
Best Local Similarity 37.9%; Pred. No. 9.5e-16;
Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 4 WGEFQVAGRSAGCGQTSNDAAAEALNASSKEALQIREKIPEKYLFOFHNLSNLDRI 63
DB 111 FGVSQIDGRSAGCGQTSNDAAAEALNASSKEALQIREKIPEKYLFOFHNLSNLDRI 170

QY 64 F 64
DB 171 F 171

RESULT 14
VAL1_SLVC STANDARD; PRT; 347 AA.
ID VAL1_SLVC
AC Q90XB3; Q90XC8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Oligodendrocyte transcription factor 2.
GN Olig2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21453760; PubMed=11567617;
RA Zhou Q., Choi G., Anderson D.J.;
RT "The bHLH transcription factor Olig2 promotes oligodendrocyte
RT differentiation in collaboration with NKX2.2.";
RL Neuron 31:791-807(2001).
RN [2]
RP SEQUENCE OF 99-161 FROM N.A.
RX MEDLINE=21453759; PubMed=11567616;
RA Novitch B.G., Chen A.I., Jessell T.M.;
RT "Coordinate regulation of motor neuron subtype identity and
RT pan-neuronal properties by the bHLH repressor Olig2.";
RL Neuron 31:773-789(2001).
CC -!- FUNCTION: Required for oligodendrocyte and motor neuron
CC specification in the spinal cord (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF411041; AAL11883.1; -.
CC EMBL; AF405699; AAL02428.1; -.
CC InterPro; IPR001092; HLH_basic.
CC Pfam; PF00010; HLH; 1.
CC SMART; SM00353; HLH; 1.
CC PROSITE; PS00038; HLH 1; 1.
CC PROSITE; PS50888; HLH 2; 1.
CC Transcription regulation; DNA-binding; Nuclear protein.
KW DNA_BIND 107 118
FT DOMAIN 119 160 BASIC DOMAIN.
FT DOMAIN 24 42 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 45 92 GLY-RICH.
FT DOMAIN 55 92 SER-RICH.
SQ SEQUENCE 298 AA; 30319 MW; 5790A79F2764F5D8 CRC64;

Query Match 18.1%; Score 65.5; DB 1; Length 298;
Best Local Similarity 32.2%; Pred. No. 5;
Matches 19; Conservative 13; Mismatches 20; Indels 7; Gaps 1;

QY 17 GCQTSNDAAAEALNASSK-----EALQIREKIPEKYLFOFHNLSNLDRI 68
DB 76 GFKSSSSASSASSASSKDKQKQTEPELQURLKINSRKRMHDLNIMDGLREVMP 134

Search completed: December 23, 2003, 08:57:40
Job time : 5.77778 secs
```


QY 1 TLVWGFOVAGRSARGGCOOTSNDAAEAALNASSKEEALQITREKIPKYLQFHNLSNL 60

DR	PRINTS; PR00227; GEMCOATALL.
DR	ProdOm; PD000736; Gemini_ALL; 1.
FT	NON TER 236 226

```

SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;
Query Match 79.6%; Score 288; DB 12; Length 226;
Best Local Similarity 80.0%; Pred. No. 4.8e-25;
Matches 56; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db 111 TVWGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 170

Qy 61 DRIPDKTPEP 70
Db 171 DRIPAKAPEP 180

RESULT 6
Q67574 PRELIMINARY; PRT; 361 AA.
AC Q67574;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative replicative protein.
GN ALI.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration.";
RL Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
RT hybridization probes and aspects of bean golden mosaic in Brazil.";
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus.";
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M86866; AAA46312.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 79.0%; Score 286; DB 12; Length 361;
Best Local Similarity 79.1%; Pred. No. 1.4e-24;
Matches 53; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 4 WGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 63
Db 113 WGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 172

Qy 64 FDKTPEP 70
Db 173 FTKAPDP 179

RESULT 7
Q9QDB1 PRELIMINARY; PRT; 225 AA.
AC Q9QDB1;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative replicative protein.
GN ALI.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration.";
RL Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
RT hybridization probes and aspects of bean golden mosaic in Brazil.";
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus.";
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M86866; AAA46312.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 79.0%; Score 286; DB 12; Length 361;
Best Local Similarity 79.1%; Pred. No. 1.4e-24;
Matches 53; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 4 WGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 63
Db 113 WGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 172

Qy 64 FDKTPEP 70
Db 173 FTKAPDP 179

RESULT 8
Q9ELT8 PRELIMINARY; PRT; 314 AA.
AC Q9ELT8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Replication association protein.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF298227; AAG01006.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 78.5%; Score 284; DB 12; Length 314;
Best Local Similarity 82.4%; Pred. No. 2e-24;
Matches 56; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db 110 TLVWGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 169

```

```

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Replication associated protein (fragment).
GN REP.
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RT Brazil.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF198708; AAF06318.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 225 225
SQ SEQUENCE 225 AA; 25766 MW; 1089CB6BD8D15B5D CRC64;

Query Match 78.5%; Score 284; DB 12; Length 225;
Best Local Similarity 79.1%; Pred. No. 1.4e-24;
Matches 53; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 4 WGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 63
Db 113 WGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 172

Qy 64 FDKTPEP 70
Db 173 FTKPPEP 179

RESULT 8
Q9ELT8 PRELIMINARY; PRT; 314 AA.
AC Q9ELT8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Replication association protein.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF298227; AAG01006.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 78.5%; Score 284; DB 12; Length 314;
Best Local Similarity 82.4%; Pred. No. 2e-24;
Matches 56; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db 110 TLVWGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 169

```

```

QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 9
Q9Q55 PRELIMINARY; PRT; 364 AA.
AC Q9Q55;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RL States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RT virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0(1999).
DR EMBL; AF104036; AAD4173.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 78.5%; Score 284; DB 12; Length 364;
Best Local Similarity 82.4%; Pred. No. 2.4e-24;
Matches 56; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGFQVAGRSARGCGCOTSDNAAAEALNASSKEALQIIRKIPKYLFOFHNLSNL 60
Db 110 TIWGFQVAGRSARGCGCOTSDNAAAEALNASSKEALQIIRKIPKYLFOFHNLSNL 169

QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA Roye M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RT "Genetic diversity among geminiviruses associated with the weed
RT species Sida spp, Macroptilium lathyroides, and Wissadula amplissima
RT from Jamaica.";
RL Plant Dis. 81:1251-1258(1997).
DR EMBL; U67926; AAB97865.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.

Query Match 76.5%; Score 277; DB 12; Length 235;
Best Local Similarity 76.1%; Pred. No. 9.2e-24;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 4 WGEFQVAGRSARGCGCOTSDNAAAEALNASSKEALQIIRKIPKYLFOFHNLSNL 63
Db 113 WGFQVAGRSARGCGCOTSDNAAAEALNASSKEALQIIRKIPKYLFOFHNLSNL 172

QY 64 FDKTPEP 70
Db 173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

```

RT "Characterization and genetic diversity of PYMV from the Caribbean.;"
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY126611; AM95995.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; Gemini_AL1; 1.
 FT NON TER 208 208
 SQ SEQUENCE 208 AA; 23667 MW; 51211D58PAD690A6 CRC64;
 Query Match 76.2%; Score 276; DB 12; Length 208;
 Best Local Similarity 72.9%; Pred. No. 1e-23;
 Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
 QY 1 TLVWGFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOFHNLSNL 60
 Db 110 TIWGLFQIDGRSARGGQQTSDNDAAEALNASSKEALQIIRKIPKYLFOFHNLSNL 169
 QY 61 DRIFDKTPEP 70
 Db 170 DRIFMKAPKP 179
 RESULT 13
 Q8JLY5 PRELIMINARY; PRT; 289 AA.
 AC Q8JLY5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Replication-associated protein (Fragment).
 GN AC1.
 OS Potato yellow mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10827;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;
 RT "Characterization and genetic diversity of PYMV from the Caribbean.;"
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY126610; AM95993.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; Gemini_AL1; 1.
 FT NON TER 289 289
 SQ SEQUENCE 289 AA; 32971 MW; 4ECF52F4C69C6764 CRC64;
 Query Match 76.2%; Score 276; DB 12; Length 289;
 Best Local Similarity 72.9%; Pred. No. 1.5e-23;
 Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
 QY 1 TLVWGFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOFHNLSNL 60
 Db 110 TIWGLFQIDGRSARGGQQTSDNDAAEALNASSKEALQIIRKIPKYLFOFHNLSNL 169
 QY 61 DRIFDKTPEP 70
 Db 170 DRIFMKAPKP 179
 RESULT 14
 P88975 PRELIMINARY; PRT; 149 AA.
 AC P88975;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Replication-associated protein (Fragment).
 GN AC1.
 OS Macrotilium golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=51676;

RN SEQUENCE FROM N.A.
 RC STRAIN=Jamaican;
 RA Roye M.E.;
 RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
 DR EMBL: U75278; AAB36919.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; Gemini_AL1; 1.
 FT NON TER 149 149
 SQ SEQUENCE 149 AA; 16785 MW; E4CF5EBD4C9CD508 CRC64;
 Query Match 75.4%; Score 273; DB 12; Length 149;
 Best Local Similarity 71.4%; Pred. No. 1.5e-23;
 Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
 QY 1 TLVWGFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOFHNLSNL 60
 Db 52 TIWGLFQIDGRSARGGQQTSDNDAAEALNASSKEALQIIRKIPKYLFOFHNLSNL 111
 QY 61 DRIFDKTPEP 70
 Db 112 DRIFMKDPEP 121
 RESULT 15
 Q9YLA4 PRELIMINARY; PRT; 233 AA.
 AC Q9YLA4;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Replication-associated protein (Fragment).
 GN REP.
 OS Macrotilium golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=51676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Jamaica strain 1;
 RA Roye M.E.;
 RT "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica.;"
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Jamaica strain 1;
 RA Roye M.E., McLaughlin W.A., Maxwell D.P.;
 RT "Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica.;"
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF098940; AADI7850.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; Gemini_AL1; 1.
 FT NON TER 233 233
 SQ SEQUENCE 233 AA; 26356 MW; AA490AF4D2166A02 CRC64;
 Query Match 75.4%; Score 273; DB 12; Length 233;
 Best Local Similarity 71.4%; Pred. No. 2.6e-23;
 Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
 QY 1 TLVWGFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOFHNLSNL 60
 Db 110 TIWGLFQIDGRSARGGQQTSDNDAAEALNASSKEALQIIRKIPKYLFOFHNLSNL 169
 QY 61 DRIFDKTPEP 70
 Db 170 DRIFMKDPEP 179

Search completed: December 23, 2003, 09:03:37
Job time : 25.3333 secs
